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July 16, 2003, 17:36:24 ; Search time 8.95784 Seconds (without alignments) 476.010 Million cell updates/sec
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1: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.
2: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.
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   version 5.1.6 - 2003 Compugen Ltd.
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102
1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
GenCore
Copyright (c) 1993
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No.	Score		Match Length DB ID	DB	ID	Description
-	75	73.5	245	19	AAW56296	Babesia microti BM
7	75	73.5	245	19	AAW56297	Babesia microti BM
m	75	73.5	245	20	AAY24353	Babesia microti an
4	75	73.5	245	21	AAB30202	B. microti BMNI-17
5	75	73.5	245	23	ABB88948	Babesia microti an
9	72	70.6	32	20	AAY24357	Babesia microti an
7	72	70.6	32	21	AAB30206	B. microti BMNI-17
8	72	70.6	32	23	ABB88951	Babesia microti an
6	36	35.3	150	21	AAG34732	Arabidopsis thalia
10	36	35.3	195	21	AAG28927	Arabidopsis thalia

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Thu Jul

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immunity; detection
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                                                                                  245 AA;
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Sleath PR;
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                                                      The sequence is that of a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:

(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick borne diseases (Iyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence is that of a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:

(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
 transformed cells and antibodies, useful for diagnosis of
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.
                                                                                                                                                                                                                                      Length 245;
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                                                                                                                                                                                                                                      Score 75; DB 19;
Pred. No. 7.4e-08;
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            infection and in protective vaccines
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                                  Claim 1; Page 66; 113pp; English.
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53.1%;
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96US-0723142.
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                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
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Matches 17; Conservative
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N-PSDB; AAV22747.
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                                                                                                                                                                                                                245 AA;
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01-OCT-1996;
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antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) that
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                                                                                                                                     have similar symptoms but require different treatments
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                                                                                                                                                                                                                                         Score 75; DB 19;
Pred. No. 7.4e-08;
0; Mismatches 15
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Pred. No. 7.4e-08;
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53.1%;
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Best Local Similarity 53.1
Matches 17; Conservative
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AAB3020; RESULT

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The present invention relates to novel Babesia microti antigens and the coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Babesia microti; antigen; immunogen; diagnosis; infection; vaccine; immunity; detection.
                                                                                                                                                                                                                                                                                                     New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 245;
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7.4e-08;
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Pred. No. 7.4e-
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                                                            27-JUN-2000; 2000US-0605724.
07-SEP-2000; 2000US-0656688.
10-0CT-2000; 2000US-0685436.
13-DEC-2000; 2000US-0737178.
26-FEB-2001; 2001US-0794764.
              09-MAY-2001; 2001WO-US15192
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Matches 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                              McNeill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 75; DB 21; Length 24
Pred. No. 7.4e-08;
0; Mismatches 15; Indels
                                                                                                                                                                 parasite; tick-borne illness; antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                                                                                                                B. microti BMNI-17 antigen SEQ ID NO: 32.
                                                                                                                                                                                   disease prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 13; Page 81-82; 118pp; English.
                            AAB30202 standard; Protein; 245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB88948 standard; Protein; 245 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Babesia microti antigen BMNI-17.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.5%;
Best Local Similarity 53.1%;
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                       05-APR-2000; 2000WO-US09136
                                                                                                                                                                                                                                                                                                                                                       05-APR-1999; 99US-0286488
17-MAR-2000; 2000US-0528784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                          CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Reed SG, Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-686939/67
                                                                                                                                                                 Sabesiosis; rodent
                                                                                                                                                                                     disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAC65094.
                                                                                                                                                                                                                   Babesia microti
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                                                                                                                                                                                                                                                     WO200060090-A1.
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                                                                                                12-FEB-2001
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                                                                                                                                                                                                                                                                                       12-OCT-2000
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                                                              AAB30202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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RESULT 5 ABB88948

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Homer MJ;

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from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                    New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21; I
4.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Babesia microti antigen BMNI-17 epitope repeat.
                                                                                                                                                                                          Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.6%; Score 72; DB 100.0%; Pred. No. 4.1 ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Len
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                                                                                                                                                                                        Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                   Claim 6; Page 85; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'label= Met, Ile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= Tyr, Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB88951 standard; Peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= Leu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     label= Ser,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Leu,
                                                 05-APR-2000; 2000WO-US09136
                                                                                        05-APR-1999; 99US-0286488.
17-MAR-2000; 2000US-0528784.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               label=
                                                                                                                                                                                                                               WPI; 2000-686939/67.
                                                                                                                                                   (CORI-) CORIXA CORP
                                                                                                                                                                                            Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 AA;
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            12-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                        Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 8
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 encode specifically claimed B. microti immunogenic proteins, and AAY24327 to AAY24338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence represents a B.microti antigen BMNI-17 degenerate repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              present invention describes isolated polypeptides comprising cific immunogenic portions of Babesia microti. AAX88993 to AAX88994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          parasite; tick-borne illness; antigen; disease prevention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 20; L
4.1e-08;
thes 0;
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Pred. No. 4.16
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Babesia microti polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 90; 126pp; English
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                                                 Val
                                                                                                                                                                      Leu
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100.08;
100.001
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/label= Ile,
21
                                                                                                                                                                                                                                                                                         /label= Cys,
                                                                                                                               label= Met,
                                                                                                                                                                                                           label= Val,
                                                                                                                                                                                                                                                  label= Thr,
                                                 label- Ala,
                                                                                        label= Leu,
                                                                                                                                                                      label- Ser,
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Best Local Similarity 100.
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MAYO-) MAYO FOUNDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORI-) CORIXA CORP.
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disease diagnosis;
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                              Misc-difference
                                                                   Misc-difference
                                                                                                        Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                          11-DEC-1998;
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Sleath PR;

Sequence

/label= Leu, Pro

Val

'label- Ala,

label= Ile,

Misc-difference Misc-difference

Babesia microti WO200060090-A1

AAB30206;

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99US-0128234.
99US-0128714.
99US-0129845.
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                            2000EP-0301439
                                                                 99US-0123180
99US-0123548
                                                                                            99US-0125788
                                                                                                           99US-0126264
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99US-0127462
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                            25-FEB-2000;
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06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                                                                                                                                                                                                                                                                           Homer MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
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                                                                                                                                                                                                                                                                                                                                                          McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 70.6%; Score 72; DB 23; Length 32; Best Local Similarity 100.0%; Pred. No. 4.1e-08; Matches 32; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 42309.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Page 91; 195pp; English.
                                                                                            'label= Thr, Ile
                                                                                                                       /label= Cys, Tyr
                                                                                                                                                                                                                              10-MAY-2000; 2000US-0569098.
27-JUN-2000; 2000US-0565724.
07-SEP-2000; 2000US-0556688.
10-OCT-2000; 2000US-0585436.
13-DEC-2000; 2000US-0791778.
26-FEB-2001; 2001US-0794764.
              /label= Met,
                                       /label= Ser,
                                                                 label= Val,
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                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-216691/27.
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Misc-difference 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 AA;
                         Misc-difference
                                                    Misc-difference
                                                                              Misc-difference
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Secrist H;
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99us-0155486

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                  35.3%; Score 36; DB 2
43.8%; Pred. No. 7.7;
tive 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG28927 standard; Protein; 195 AA
990S-0155659.
990S-0156458.
990S-0156458.
990S-015753-
990S-0158029.
990S-0158029.
990S-0158029.
990S-0159294.
990S-0159294.
990S-015930.
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Best Local Similarity 43.8
Matches 7; Conservative
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05-MAR-1999;
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16 JUL 1999; 19 JUL 1999; 19 JUL 1999; 19 JUL 1999; 19 JUL 1999; 19 JUL 1999; 20 JUL 1999; 20 JUL 1999; 21 JUL 1999; 22 JUL 1999; 22 JUL 1999; 23 JUL 1999; 23 JUL 1999; 23 JUL 1999; 24 JUL 1999; 25 JUL 1999; 27 JUL 1999; 28 JUL 1999; 29 JUL 1999; 20 AUG 1999; 20 AUG 1999; 21 AUG 1999; 21 JUL 1999; 22 JUL 1999; 23 JUL 1999; 23 JUL 1999; 24 JUL 1999; 25 JUL 1999; 26 JUL 1999; 27 JUL 1999; 27 JUL 1999; 28 JUL 1999; 29 JUL 1999; 20 AUG 1999; 21 AUG 1999; 21 AUG 1999; 22 AUG 1999; 23 AUG 1999; 24 AUG 1999; 25 AUG 1999; 26 AUG 1999; 27 AUG 1999; 27 AUG 1999; 28 AUG 1999; 28 AUG 1999; 29 AUG 1999; 20 AUG 1999; 20 AUG 1999; 20 AUG 1999;	23-AUG-1999) 25-AUG-1999) 27-AUG-1999) 27-AUG-1999) 37-AUG-1999) 31-AUG-1999) 31-AUG-1999) 31-SEP-1999) 15-SEP-1999) 15-SEP-1999) 22-SEP-1999) 23-SEP-1999) 24-SEP-1999) 26-CGT-1999) 66-OCT-1999)
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23-MAR-1999; 25-MAR-1999; 06-APR-1999; 06-APR-1999; 06-APR-1999; 19-APR-1999; 19-APR-1999; 23-APR-1999; 23-APR-1999; 23-APR-1999; 06-MAY-1999; 06-MAY-1999; 11-MAY-1999; 11-MA	18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 18-UN-1999; 23-UN-1999; 23-UN-1999; 23-UN-1999; 24-UN-1999; 24-UN-1999; 26-UN-1999; 01-UL-1999; 01-UL-1999; 06-UL-1999; 06-UL-1999; 13-UL-1999; 11-UL-1999; 11-UL-1999; 11-UL-1999; 11-UL-1999; 11-UL-1999; 11-UL-1999; 11-UL-1999; 11-UL-1999; 11-UL-1999; 11-UL-1999; 11-UL-1999;
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2000US-235484P.
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2000US-236327P.
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2000US-218290P
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14-JUL-2000; 2
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14-AUG-2000; 2
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                                                         99US-0159293.
99US-0159294.
99US-0159295.
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2000US-180628P.
2000US-184664P.
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99US-0159330.
99US-0159331.
99US-0159637.
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99US-0159584.
99US-0160741.
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2000US-205515P.
2000US-209467P.
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99US-0160814
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99US-0162142
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                                                                                                                                                                                                                                                            99US-01607
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Best Local Similarity 43.8
Matches 7; Conservative
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24-FEB-2000;
02-MAR-2000;
16-MAR-2000;
17-MAR-2000;
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18-0cr-1999
21-0cr-1999
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25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
26-0CT-1999;
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19-MAY-2000;
07-JUN-2000;
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                                                                      DB 22;
                                                                  Score 35; DB 2
Pred. No. 8;
2; Mismatches
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                                                              34.3%;
nilarity 54.5%;
Conservative 2
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   Sequence
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N-PSDB; ABA06573.
               20-0CT-2000
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The present invention relates to the isolation of novel human uterine motility-association polypeptides, and cDNA (AAS28936-AAS28994) and genomic sequences encoding for these polypeptides.

The sequences of the invention are useful in the diagnosis, treatment, prevention and/or prognosis of diseases associated with uterine motility such as pregnancy and labour, and menstrual disorders. The polynucleotide sequences of the invention are also useful in gene therapy. AAU18094-AAU18152 represent novel human uterine motility-association polypeptides.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated polypeptide and nucleic acid molecules for treating, preventing and/or prognosing disorders related to uterine motility e.g. disorders associated with pregnancy and the menstrual cycle-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11; SEQ ID No 108; 524pp; English.
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2000US-0251030.
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Matches 6; Conservative
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2000US-0234274.
2000US-0234997.
2000US-0234998.
2000US-0235484.
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2000US-0233065
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08-DEC-2000;
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       vulnerary; secreted protein; rheumatoid arthritis; hyperproliferative disorder; cardiovascular disorder; cardiovascular disorder; carebral ischaemia; angiogenesis; nervous system disorder; hiperproliferation; ocular disorder; corneal infection; wound healing; epithelial cell proliferation; skin ageing; food additive; preservative; antiproliferative.
neuroprotective; antibacterial; virucide; fungicide; opthalmalogical;
                                                                                                                     17-JAN-2001; 2001WO-US01320
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2000US-0232401
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                                                                                  WO200155441-A2.
                                                                    Homo sapiens
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07-JUN-2000;
28-JUN-2000;
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07-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to isolated nucleic acid molecules and their encoded secreted proteins. The nucleic acids and proteins are used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnoshing a pathological condition or susceptibility to a pathological condition. Antibodies to the proteins can also be used in alleviating symptoms associated with the disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays (ELISA). Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, choperproliferative disorders e.g. recubrassis of the breast or liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, serebrovascular disorders e.g. cardiac arrest, viruses and fungi and ocular disorders e.g. corneal infection, and many other disorders e.g. corneal infection, and many other and would healing and epithelial cell.proliferation, to convent ell manner before convented to the convented of the convented 
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                                                                                                                                                                                                                                                                                                                                                              Novel polypeptides and polynucleotides useful as diagnostic reagents to
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                                                                                                                                                                                                                                                                                                                                                                                           diagnose diseases or disorders associated with aberrant expression or activity of polypeptides, for treating blood clotting disorder,
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Pred. No.
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54.5%;
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08-DEC-2000; 2000US-0251868.
08-DEC-2000; 2000US-0251865.
08-DEC-2000; 2000US-0251989.
08-DEC-2000; 2000US-0251990.
11-DEC-2000; 2000US-0254097.
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N-PSDB; AAS26950.
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Best Local Similarity
Matches 6; Conserv
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Barash SC, Ruben SM;
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                            29 SEP - 2000, 202 - CCT - 200
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The present invention relates to the isolation of novel human calcium-binding proteins, and cDNA (AAS31577-AAS31654) and genomic sequences encoding for these proteins. The sequences of the invention are useful in the diagnosis, prevention and/or prognosis of diseases associated with aberrant calcium flux. Such disorders include neurological diseases (e.g. amylotrophic lateral sclerosis, ALS), immune dysfunction (e.g. severe combined immunodeficiency, SCID), disease (e.g. cancer), blood disorders (e.g. irritable bowel syndrome, IBS), neoplastic disease (e.g. acquired immunodeficiency syndrome, ALDS). The novel calcium-binding proteins are also useful as screening tools to infectious disease (e.g. acquired immunodeficiency syndrome, ALDS). The novel calcium-binding proteins are also useful as screening tools to identify antagonists and/or agonists that may enhance or inhibit activities mediated by calcium-binding proteins. The polynucleotides of the invention are also useful in gene therapy. AV(19892-AA(1969) represent the novel human calcium-binding proteins.

Specification, but was obtained in electronic format directly from WIPO
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                                                                         Isolated nucleic acid molecule encoding a calcium-binding protein is used in preventing, treating or ameliorating a medical condition
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tissue regeneration; wound healing; infection; immune disorder;
cell culture; drug screening; ger therapy; antiinflammatory;
antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
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                                                                                                                                                             Claim 11; SEQ ID No 94; 542pp; English
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27-APR-2000; 2000US-0560875.
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                            N-PSDB; AAS31582
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Matches
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(HYSE-) HYSEQ INC.
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Tang YT, Liu C, Drmanac RT;

WPI; 2001-457740/49.

N-PSDB; ABA08648.

Human proteins and DNA encoding sequences useful for preventing, treating or ameliorating a medical condition in a mammalian subject e.g. arthritis and cancer -

Claim 20; Page 179-181; 1963pp; English.

Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and sequences ABB10981-ABB12330 represent nucleat caids encoding them. The invention also relates to vectors and recombinant host cells comprising a nucleicide of the invention, methods of producing the novel polypeptides of the invention. Although novel, many of the nucleotides or polypeptides in a sample, and methods of identifying compounds which bid bid to polypeptides of the invention. Although novel, many of the polypeptides of the invention have homology to known proteins, thereby giving an insight into their probable biological activities, and hence potential thesapeutic applications. The polypeptides of the invention may have various activities; stem cell growth factor activity; therethy differentiation activities; stem cell growth factor activity; hammunomodulatory activity; activin. or inhibin-related activities; chemotactic or chemokinetic activities; propaptides and nucleotides of the invention are useful for preventing, treating or mationating medical involved in oncogenesis, cancer cell proliferation or metastasis.

Depending on their biological activities, polypeptides and nucleotides of the invention are useful for preventing, treating or amaliorating medical cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell disorders, chronic inflammatory conditions (e.g., asthma or arthritis), arschamia, bone disorders (e.g., osteoporosis), and abnormal disorders (e.g., of burns, incisions and ulcers), while those with immunomodulatory activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders activities may be used in the treatment of viral, bacterial and fungal infections in addition to immune disorders call growth. For example, such polypeptides may be used to manipulate stem cells in culture to give rise to neuroepithelial cells autoprices are dispersed in the diagnosis of the cape to admine or replace cell growth. For example, such polypeptides and nucleotides may ac

Sequence 2560 AA;

Query Match 34.3%; Score 35; DB 22; Length 2560; Best Local Similarity 54.5%; Pred. No. 2.2e+02; Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps

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1 RCLSIXRFXXS 11 | | | | |

QY Db

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Sequence 25,
Sequence 2,
Sequence 1,
Sequence 4,
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5: SEED AND BERRY
6300 Columbia Center, 701 Fifth Avenue
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Pred. No. 7.7e-08;
                                                                    US-08-467-9488-30
US-08-467-9488-30
US-08-467-9478-30
US-08-677-9488-8
US-08-467-9478-8
US-08-467-9478-8
US-08-417-1218-6
US-08-417-122-6
US-08-417-122-6
US-08-417-122-6
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US-08-541-759B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 32, Application US/08845258 Patent No. 6183976 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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STATE: Washington
COUNTRY: USA
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Best Local Similarity
Matches 17; Conserv
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being printed,
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/cgn2_6/ptodata/1/iaa/PcTUS_COMB.pep:*
                      GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd
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US-09-574-141A-66
US-09-081-320-3
US-09-574-141A-3
US-09-574-141B-3
US-08-707-780-3
US-08-175-18
US-08-11S-682A-2
US-08-11S-682A-2
US-08-11S-685-5
US-08-615-203-2
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US-08-616-241-5
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1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
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US-09-52B-784A-32
US-08-845-25B-36
US-08-990-571-36
US-08-723-142A-36
US-09-52B-784A-36
US-09-52B-694A-4
US-08-878-283-4
US-09-574-141A-64
US-09-574-141A-64
US-09-574-141A-64
US-09-574-141A-64
US-08-852-824-17
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                           protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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length: 2000000000
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Match
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Score

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Scoring table:

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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: General Research Compounds AND TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.42664
CURRENT APPLICATION NUMBER: US/09/528.784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                Score 75; DB 4; Length 245;
Pred. No. 7.7e-08;
0; Mismatches 15; Indels
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PatentIn Release #1.0, Version #1.30
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53.1%; Pred. No. 7.7e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 36, Application US/08845258 Patent No. 6183976
                                                                             CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                           REFERENCE, DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206)682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                     73.5%;
53.1%;
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
                                                          01-0CT-1996
                                                                                                                                                                                                                                                                                         LENGTH: 245 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 73.55
Best Local Similarity 53.15
Matches 17; Conservative
                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE: 01-OCT-15
                                                                                                                                                                                                                          TELEFAX: (206)682-6031 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 73.5
Best Local Similarity 53.1
Matches 17; Conservative
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                                                                                                                                                                                                                                                                                                                 amino acid
                                                                                                                                                                                                                                                                                                                                                            linear
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TOPOLOGY: 1in

US-08-723-142A-32
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                                                                     Sequence 32, Application US/08990571
Patent No. 6214971
GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION:
COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.
NUMBER OF SEQUENCES: 79
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                            ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
FILLING DATE: US/08/990,571
FILLING DATE: 11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 75; DB 4;
Pred. No. 7.7e-08;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 32, Application US/08723142A Patent No. 6306396
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ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPATIBLE
PC-DOS/MS-F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 245 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 73.55
Best Local Similarity 53.15
Matches 17; Conservative
                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: SEED AND STREET: 6300 Columb CITY: Seattle STATE: Washington
                                                                                                                                                                                                                                                                                       STATE: Washington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                98104
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US-08-723-142A-32
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US-08-990-571-32
                                                        US-08-990-571-32
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us-09-853-079-36.rai

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LOCATION: 20
OTHER INFORMATION: /note= "Residue can be either lle
OTHER INFORMATION: or Phe"
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LOCATION: 21
OTHER INFORMATION: /note= "Residue can be either Ala
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OTHER INFORMATION: or Ile"
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OTHER INFORMATION: or Ser"
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OTHER INFORMATION: or Ile"
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OTHER INFORMATION: or Arg"
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                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Elab PC compatible
COMPUTER: Elab PC compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION NUMBER: 31,392
ATORNEY/AGENT INFORMATION:
NAME: MAIL, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/POCKET UNMBER: 210121.426C1
TELECOMMULCATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFRA: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: /note= "Residue can be either OTHER INFORMATION: or Phe"
                               E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "Residue can be Pro,
Leu"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Modified-site LOCATION: 17
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CORRESPONDENCE ADDRESS:
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                          CITY: Seattle
STATE: Washington
                                                                                                                                                                COUNTRY: U
ZIP: 98104
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APPLICANT: Reed, Steven G. et al.

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF
NUMBER OF SEQUENCES: 79
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                                                                             /note= "Residue can be either Leu
or Pro"
                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site
LOCATION: 28
OTHER INFORMATION: /note= "Residue can be either Val
OTHER INFORMATION: or Phe"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; OTHER INFORMATION: /note= "Residue can be either Cys; OTHER INFORMATION: Or Tyr" US-08-845-258-36
                                                                                                                                                                LOCATION: 26
OTHER INFORMATION: /note= "Residue can be either Met
OTHER INFORMATION: or Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "Residue can be either Thr
or Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER FIGURAL FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: TBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
FILING DATE: II-DEC-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MAK!, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 210121.426C2
TELECOMMUNICATION IFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                          /note= "Residue can be either or Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
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OTHER INFORMATION: or Val"
                                                                                                                                                                                                                                              NAME/KEY: Modified-site
LOCATION: 27
OTHER INFORMATION: /note=
OTHER INFORMATION: or Leu'
FEATURE:
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LOCATION: 29
OTHER INFORMATION: /note
OTHER INFORMATION: or il
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NAME/KEY: Modified-site
LOCATION: 30
                                       Modified-site
                                                                                                                                             NAME/KEY: Modified-site
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Best Local Similarity 100.0
Matches 32; Conservative
                                                                               OTHER INFORMATION:
OTHER INFORMATION:
EATURE:
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US-08-990-571-36
                                                               LOCATION:
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/note= "Residue can be Glu, Asp or Gly"
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or Ile"
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or Pro"
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or Val"
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or Phe"
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Leu"
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or Thr"
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                                                                                                                                                                                                                                                      or Ser"
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NAME/KEY:
MODIFIED 17
LOCATION: 17
OTHER INFORMATION: Or Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY:
MODIFIED-SITE
LOCATION: 19
OTHER INFORMATION: /note-
OTHER INFORMATION: Gly"
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LOCATION: 20
OTHER INFORMATION: /note=
OTHER INFORMATION: or Phe
FEATURE:
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NAME/KEY: Modified-site
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LOCATION: 10
OTHER INFORMATION: /note
OTHER INFORMATION: or Ph
                                                                                                                NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /note
OTHER INFORMATION: Or Il
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LOCATION: 13
OTHER INFORMATION: /note
OTHER INFORMATION: Leu"
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NAME/KEY: Modified-site
LOCATION: 26
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LOCATION: 28
OTHER INFORMATION: /note
OTHER INFORMATION: or Ph
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acids
STRANDEDNESS:
                                                                                                                                                                                                                               OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
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OTHER INFORMATION:
FEATURE:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
                                                                                    TOPOLOGY: linear
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
                                                                                                                                                                                                                    Ouery Match 70.6%; Score 72; DB 4; Length 32; Best Local Similarity 100.0%; Pred. No. 4.1e-08; Matches 32; Conservative 0; Mismatches 0; Indels
               /note= "Residue can be either Thror Ile"
                                                                                                                      /note= "Residue can be either Cys
or Tyr"
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or Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,142A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MAK1, David J.
REGISTRATION NUMBER: 31.392
REGISTRATION NUMBER: 31.392
REGISTRATION NUMBER: 210121.426
TELEFONGET (206) 622-4900
TELEFONGET (206) 622-4900
TELEFNX: (206) 682-4601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6300 Columbia Center, 701 Fifth Avenue
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                                                                                                                                                                                                                                                                                                           1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
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LOCATION: 29
COTHER INFORMATION: /note==
COTHER INFORMATION: or Ile*
FEATURE:
NAME/KEY: Modified-site
LOCATION: 30
COTHER INFORMATION: /note==
COTHER INFORMATION: or Tyr*
US-08-990-571-36
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NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: Or Ser
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10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-723-142A-36
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: McNeill, Particia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C4
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: PRESENTED FOR MINDOWS SECOND NOS SECOND N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (6)...(6)
OTHER INFORMATION: Xaa = Methionine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa - Serine or Phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: VARIANT
LOCATION: (12)...(12)
OTHER INFORMATION: Xaa = Leucine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (9)...(9)
OTHER INFORMATION: Xaa = Tyrosine or Serine
                                                                     Sequence 36, Application US/09528784A Patent No. 6451315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Babesia microti
                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Reed, St
APPLICANT: Lodes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
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                                  -09-528-784A-36
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 20
OTHER INFORMATION: /note= "Residue can be either Ile
OTHER INFORMATION: or Phe"
OTHER INFORMATION: /note= "Residue can be either Ser
OTHER INFORMATION: or Phe"
                                                                                                                                                                             OTHER INFORMATION: /note= "Residue can be either Leu
OTHER INFORMATION: or Ile"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "Residue can be either Ala OTHER INFORMATION: or Val"
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OTHER INFORMATION: or Pro"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Residue can be either Met
or Thr"
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OTHER INFORMATION: /note= "Residue can be either Ser
OTHER INFORMATION: or Leu"
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LOCATION: 28
OCHER INFORMATION: /note= "Residue can be either Val
OTHER INFORMATION: or Phe"
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or Ile"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Residue can be either Leu
or Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: /note- "Residue can be Glu, Asp OTHER INFORMATION: \text{Gly}^{\text{\tiny{I}}}
                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: /note= "Residue can be Pro, OTHER INFORMATION: Leu"
                                                                                                       NAME/KEY: Modified-site LOCATION: 12
                                                                                                                                                                                                                                                          FEATURE: Nodified-site
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NAME/KEY: Modified-site
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY:
LOCATION:
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LOCATION:
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Gaps
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LOCATION: (19)...(19)
OTHER INFORMATION: Xaa - Glutamic Acid, Aspartic Acid or Glycine
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                                                                                                                                                                                                                           NAME/KEY: VARIANT LOCATION: (20)...(20) OTHER INFORMATION: Xaa = Isoleucine or Phenylalanine
NAME/KEY: VARIANT
LOCATION: (13)
OTHER INFORMATION: Xaa = Proline, Serine or Leucine
NAME/KEY: VARIANT
LOCATION: (17)...(17)
OTHER INFORMATION: Xaa = Leucine or Arginine
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Best Local Similarity 100.0%; Pred. No. 4.1e-08;
Matches 32; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
LOCATION: (28)...(28)
OTHER INFORMATION: Xaa = Valine or Phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (26)...(26)
OTHER INFORMATION: Xaa = Methionine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT LOCATION: (29)...(29) OTHER INFORMATION: Xaa = Threonine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (30)...(30)
CTHER INFORMATION: Xaa = Cysteine ro Tyrosine US-09-528-784A-36
                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (23)...(23)
OTHER INFORMATION: Xaa = Leucine or Proline
                                                                                                                                                                                                                                                                                                       NAME/KEY: VARIANT
LOCATION: (21)...(21)
OCHER INFORMATION: Xaa - Alanine or Valine
NAME/KEY: VARIANT
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OTHER INFORMATION: Xaa = Serine or Leucine
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REFERENCE/DOCKET NUMBER: OMRF152
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
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Best Local Similarity
Matches 7; Conserva
                                                                                              OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
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Patent No. 5852171
GENERAL INFORMATION:
APPLICANT: Fukudome, Kenji
APPLICANT: Esmon, Charles T.
TITLE OF INVENTION: Cloning and Regulation of an Endothelial
TITLE OF INVENTION: Call Protein C/Activated Protein C Receptor
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                Sequence 4, Application US/08289699A
Patent No. 569593
GENERAL INFORMATION:
APPLICANT: Fukudome, Kenji
APPLICANT: Esmon, Charles T.
TITLE OF INVENTION: Cloning and Regulation of an Endothelial
TITLE OF INVENTION: Cell Protein C/Activated Protein C Receptor
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                                                                                                                                                                                                                                                                                                                                     STREET: 2800 One Atlantic Center, 1201 West Peachtree STREET: Street
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STREET: 2800 One Atlantic Center, 1201 West Peachtree
STREET: Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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30;
RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                  1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXFL 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/289,699A FILLING DATE: 12-AUG-1994 CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGIESTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
STATE: Georgia
COUNTRY: US
ZIP: 33306-3450
COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
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Patent No. 6399064
GENERAL INFORMATION:
APPLICANT: Fukudome, Kenji
APPLICANT: Fukudome, Kenji
TITLE OF INVENTION: Cloning and Regulation of an Endothelial
Cell Protein C/Activated Protein C Receptor
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ADDRESSEE: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1201 West Peachtree
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                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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FILING DATE: 29-Oct-1998
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/878,283
                                                                                                                                                FILING DATE:
CLASSIFCRATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,699
FILING DATE: 12-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
                                                                                                                               APPLICATION NUMBER: US/08/878,283
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ZIP: 30306-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ATTORNEY/AGENT INFORMATION:
                                           IBM PC compatible
                                                                                                                                                                                                                                                                                                   31,284
                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION TELEPHONE: (404)873-8794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 32.4%;
50.0%;
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                NAME: Pabst, Patrea L. REGISTRATION NUMBER: 31, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 (404)873-8794
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
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                                               DB 3; Length 348;
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Patent No. 6043351
GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
TITLE OF INVENTION: EPSTEIN BARR VIRUS INDUCED GENES
CORRESPONDENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
CITY: Boston
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Epstein Barr Virus Induced Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION PC-DOS/MS-DOS
CURRENT APPLICATION Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,750
FILING DATE: Herewith
CLASSIFICATION: 43f
ATTORNEY/APPLICATION: 43f
                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Birkenbach, Mark
APPLICANT: Birkenbach, Mark
APPLICANT: Birkenbach, Mark
APPLICANT: Birkenbach, Mark
APPLICANT: Birkenbach:
INIMER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, N.W.,
STREET: Suite 600
CITY: Washington
STATE:
                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0627.3300001
                                               Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Fox, Samuel, L.
REGISTRATION NUMBER: 30,353
REFERENCE/DOCKET NUMBER: 0627
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                      US-08-383-750-4; Sequence 4, Application US/08383750; Patent No. 5744301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
                                          Query Match 30.4%;
Best Local Similarity 85.7%;
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 85.7
Matches 6; Conservative
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US-08-852-824-17
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0
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APPLICANT: Gonsalves, Dennis
APPLICANT: Gonsalves, Dennis
APPLICANT: Gonsalves, Dennis
APPLICANT: Med, Baozhons
ITILE OF INVENTION: WUEBETRIS STEM PITTING ASSOCIATED VIRUS
ITILE OF INVENTION: NUCLEIC ACIDS, PROTEINS, AND THEIR USES
FILE REPERRENCE: 07678/035005
CURRENT APPLICATION NUMBER: 05/09/574,141A
CURRENT APPLICATION NUMBER: 60/047,147
PRIOR FILING DATE: 1997-05-20
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/069,902
PRIOR APPLICATION NUMBER: 60/069,902
PRIOR APPLICATION NUMBER: 09/081,320
PRIOR APPLICATION NUMBER: 09/081,330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB 4; Length 379;
Pred. No. 34;
                                                                                                                                                                                                                                                                                                             DB 4; Length 335; 30;
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                                                                                                                                                                                                                                                                                                                                                               7; Indels
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TITLE OF INVENTION: Human G-Protein Coupled Receptors
FILE REFERENCE: 1488.1220000
CURRENT APPLICATION NUMBER: US/08/852,824C
CURRENT FILING DATE: 1997-05-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Rupestris stem pitting associated virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match 32.4%; Score 33; DB ABest Local Similarity 33.3%; Pred. No. 34; Matches 7; Conservative 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                               Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 17, Application US/08852824C Patent No. 6060272 GENERAL INFORMATION:
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US-09-574-141A-64
: Sequence 64, Application US/09574141A
; Patent No. 6395490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              228 AIMRESGEASTFLNTLANMLF 248
TELECOMMUNICATION INFORMATION
                    TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 4:
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                                                                                                              LENGTH: 335 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                             32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                            1 RCLSIXRFXXSXXT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                       29 RCLQISSFANSSWT 42
                                                                                                                                                                                                                                                                                                                                                               7; Conservative
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Matches 7; Conserva
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ORGANISM: genomic
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LENGTH: 348
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COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: IFOLOPY disk
COMPUTER: INM PC compatible
COMPUTER: APPLICATION NUMBER: US/08/352,678
FILING DATE: 25-NOV-1994
FILING DATE: 25-NOV-1994
FILING DATE: 25-NOV-1992
FILING DATE: 35-NOV-1992
FILING DATE: 31-616
FILING DATE: 25-NOV-1992
FILING DATE: 31-616
FILING DATE: 25-NOV-1992
FILING DATE: 25-NOV-1993
FILING DATE: 30-NOV-1993
FILING
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July 16, 2003, 17:47:39 ; Search time 5.2344 Seconds (without alignments) 726.026 Million cell updates/sec
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/cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMD.pep: *
/cgn2_6/ptodata/2/pubpaa/NCSO7_PUBCOMD.pep: *
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/cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep: *
0: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep: *
1: /cgn2_6/ptodata/2/pubpaa/USO9_NEW_PUB.pep: *
2: /cgn2_6/ptodata/2/pubpaa/USO1_PUBCOMB.pep: *
2: /cgn2_6/ptodata/2/pubpaa/USO1_PUBCOMB.pep: *
3: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep: *
4: /cgn2_6/ptodata/2/pubpaa/USO0_NEW_PUB.pep: *
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/cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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102
1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451899 seqs, 118759770 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                                            OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                              Title:
Perfect score:
Sequence:
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		Description	Sequence 32, Appl	Sequence 32, Appl	Sequence 32, Appl	Sequence 36, Appl	Sequence 36, Appl	Sequence 36, Appl	Sequence 108, App	Sequence 94, Appl	Sequence 659, App	Sequence 286, App	Sequence 3, Appli	Sequence 524, App	Sequence 4, Appli	Sequence 2, Appli	Sequence 996, App	Sequence 12232, A	Sequence 27, Appl	Sequence 444, App	Sequence 2, Appli
SOMESTICS	4	LD	US-09-286-488-32	US-09-853-079-32	US-09-737-178-32	US-09-286-488-36	US-09-853-079-36	US-09-737-178-36	US-10-073-865-108	US-09-764-881-94	US-09-764-853-659	US-09-764-898-286	US-09-916-849A-3	US-10-225-567A-524	US-09-788-711A-4	US-09-788-711A-2	US-09-764-864-996	US-10-156-761-12232	US-09-737-149-27	US-10-225-567A-444	US-09-737-149-2
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	1	Match Length DB	245	245	245	32	32	32	96	96	96	96	2923	2923	2923	2956	359	1039	1713	3014	3014
ď	Query	Match	73.5	73.5	73.5	9.07	70.6	70.6	34.3	34.3	34.3	34.3	34.3	34.3	34.3	34.3	33,3	32.4	31.4	31.4	31.4
		score	75	75	75	72	72	72	35	35	35	35	35	35	32	35	34	33	32	32	32
	Result		1	7	æ	4	S	9	7	80	6	10	11	12	13	14	15	16	17	18	19

Sequence 25, Appl Sequence 21, Appl Sequence 21, Appl Sequence 29, Appl Sequence 25, Appl Sequence 25, Appl Sequence 27, Appl Sequence 17, Appl Sequence 206, Appl Sequence 112, Appl Sequence 111, Appl Sequence 102, Appl Sequence 102, Appl Sequence 1, Appl Sequence 1, Appl Sequence 1, Appl Sequence 216, Appl Sequence	NC	Length 245; ; Indels 0; Gaps 0;
US-09-737-149-25 US-09-737-149-30 US-09-737-149-30 US-10-25-567A-656 US-09-738-626-5579 US-09-738-626-5579 US-09-738-626-5579 US-09-738-626-5579 US-09-738-626-5579 US-10-251-385-78 US-10-251-385-78 US-10-251-385-78 US-10-251-385-78 US-10-251-385-78 US-10-251-385-78 US-10-251-385-78 US-09-864-761-3866 US-09-864-761-3866 US-09-864-761-3866 US-09-864-761-3866 US-09-864-761-3866 US-09-862-027-81 US-09-862-027-81 US-09-862-027-81 US-09-862-027-81 US-09-862-027-81 US-09-862-027-81 US-10-074-095-306 US-10-074-095-306 US-10-106-698-5603 US-10-106-698-5603 US-10-106-698-5603	CTHODS FOR THE B. MICROTI I 6,488	imilarity 53.1%; Score 75; DB 9; Len Conservative 0; Mismatches 15; CCONSERVATIVE 0; Mismatches 15; RCLSIXREXXXXTEIXIXXXXXEE 32
3034 3034 33238 33238 33328 3312 3619 3619 3619 3619 3619 4110 7119 719 823 99 1734 10 1734 10 503 99 503 99 503 99 503 99 619 86 99 86 99	nn US/09286488 6A1 nn G. nael J. aymond L. LI R. LI R. MPOUNDS AND M DY TEATMENT C. 14262 1999-04-05 83 Windows Versi	73.5%; vative xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxx
44444444444444444555555555555555555555	-32 (Application USASO020169136A1 ORMATION: Reds, Steven G Lodes, Michael Houghton, Rayma Sleath, Paul R MCNEILI, Paul R MCNEILI, Patril NVENTION: AND TI ENCE: 210121.42 ENCE: 210121.42 ELING DATE: 1999 SEQ ID NOS: 83 EASTEED for Winn 2 Babesia microt.	h Similarity 53.15 Similarity 53.11 Sconservative 1 RCLSIXREXXSXTFI
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LON: (19)...(19)
INFORMATION: Xaa = Glutamic Acid, Aspartic Acid or Glycine
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INFORMATION: Xaa = Isoleucine or Phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ION: (13)...(13)
INFORMATION: Xaa = Proline, Serine or Leucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                  - Methionine or Isoleucine
                                                                                                                                                                                                                                                                                                                                           ION: (10)...(10)
INFORMATION: Xaa = Serine or Phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ION: (26)...(26)
INFORMATION: Xaa - Methionine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ION: (28)...(28)
INFORMATION: Xaa = Valine or Phenylalanine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (29)...(29)
OTHER INFORMATION: Xaa = Threonine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 72; DB 9; I
Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                           ION: (12)...(12)
INFORMATION: Xaa = Leucine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            70.6%; bcc. 100.0%; Pred. No. 1... 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COCATION: (30) ... (30) ... (310) ... OTHER INFORMATION: Xaa = Cysteine ro Tyrosine US-09-286-488-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ION: (17)...(17)
INFORMATION: xaa = Leucine or Arginine
                                                                                                                                                                                                                                                                                - Tyrosine or Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: (23)...(23)
OTHER INFORMATION: Xaa = Leucine or Proline

    Serine or Leucine

          NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 70.6
Best Local Similarity 100.
Matches 32; Conservative
                                                                                                              ORGANISM: Babesia microti
                                                                                                                                                                             LOCATION: (6)...(6)
OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                                             ION: (9)...(9)
INFORMATION: Xaa
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INFORMATION: Xaa
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OTHER INFORMATION: Xaa
                                                                                                                                                                                                                                     NAME/KEY: VARIANT
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                                                                                                                                                   NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT
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                                    SEQ ID NO 36
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LOCATION:
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Pred. No. 2.1e-07;
); Mismatches 15; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS-
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS-
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C11
CURRENT PEPLICATION UNMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 245
                                                                                                                                                                                                                                                                                                                         Length 245;
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: MCNEILL, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
CURRENT APPLICATION NUMBER: US/09/286,488
CURRENT FILING DATE: 1999-04-05
                                                                                                                                                                                                                                                                                                                                                                15; Indels
                                                                                                                                                                                                                                                                                                                                           2.1e-07;
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CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
                                                                                                                                                                                                                                                                                                                       Score 75;
Pred. No.
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Lodes, Michael J.
Houghton, Raymond L.
Sleath, Paul R.
McNeill, Patricia D.
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53.1%;
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Best Local Similarity 53.1
Matches 17; Conservative
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US-09-853-079-32
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US-09-737-178-32
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SOFTWARE: FastSEQ for
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Best Local Similarity
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LENGTH: 245
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APPLICANT:
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OTHER INFORMATION: Xaa = Glutamic Acid, Aspartic Acid or Glycine
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APPLICANT: Reed, Steven G.
APPLICANT: Reed, Steven G.
APPLICANT: Lodges, Michael J.
APPLICANT: Lodges, Michael J.
APPLICANT: About R.
APPLICANT: About R.
APPLICANT: Moner, Mary
APPLICANT: Moner, Mary
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROII INFECTION
FILE REFERENCE: 210121.426611
CURRENT APPLICATION NUMBER: 105/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 32
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OTHER INFORMATION: Xaa = Isoleucine or Phenylalanine
FEATURE:
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OTHER INFORMATION: Xaa = Proline, Serine or Leucine
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OTHER INFORMATION: Xaa - Methionine or Isoleucine
FEATURE:
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OTHER INFORMATION: Xaa = Methionine or Threonine
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OTHER INFORMATION: Xaa = Serine or Phenylalanine
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OTHER INFORMATION: Xaa - Leucine or Isoleucine
1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXFL 32
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OTHER INFORMATION: Xaa = Leucine or Arginine
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LOCATION: (9)...(9)
OTHER INFORMATION: Xaa - Tyrosine or Serine
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OTHER INFORMATION: Xaa = Leucine or Proline
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LOCATION: (21)...(21)
OTHER INFORMATION: Xaa = Alanine or Valine
                                                                                                                      US-09-853-079-36
; Sequence 36, Application US/09853079
; Publication No. US20030109689A1
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OTHER INFORMATION: Xaa = Glutamic Acid, Aspartic Acid or Glycine
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APPLICANT: Sleath, which is a stricted b.
APPLICANT: Mary Hearther
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE DE INVENTION: COMPOUNDS AND TREATMENT OF B. MICROII INFECTION
FILE REFERENCE: 210121.426C9
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FEASTED for Windows Version 3.0
SEQ ID NO 36
LENGTH: 32
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LOCATION: (20)...(20)
OTHER INFORMATION: Xaa = Isoleucine or Phenylalanine
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OTHER INFORMATION: Xaa = Proline, Serine or Leucine
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LOCATION: (6)...(6)
OTHER INFORMATION: Xaa = Methionine or Isoleucine
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                                                                                                                                                                                              LOCATION: (29)...(29)
CTHER INFORMATION: Xaa = Threonine or Isoleucine
FERTURE:
NAME/KEY: VARIANT
LOCATION: (30)
CTHER INFORMATION: Xaa = Cysteine ro Tyrosine
US-09-853-079-36
                                                                                                  LOCATION: (28)...(28)
OTHER INFORMATION: Xaa - Valine or Phenylalanine
FEATURE:
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OTHER INFORMATION: Xaa = Serine or Phenylalanine
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OTHER INFORMATION: Xaa - Leucine or Isoleucine
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OTHER INFORMATION: Xaa = Leucine or Arginine
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LOCATION: (9)...(9)
OTHER INFORMATION: Xaa = Tyrosine or Serine
LOCATION: (27)...(27)
OTHER INFORMATION: Xaa = Serine or Leucine
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APPLICANT: Reed, 5
                                                  FEATURE: NAME/KEY: VARIANT
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
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54.5%;
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Best Local Similarity 54.5
Matches 6; Conservative
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Matches 6; Conservative
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24 RCVSVLRFDSS 34
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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LOCATION: (89)
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LENGTH: 96
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Sequence 108, Application US/10073865

Sequence 108, Application US/10073865

Publication No. US20030044904A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE COF INVENTION: NUCleic Acids, Proteins, and Antibodies
FILE REFERENCE: PJ209C1

CURRENT APPLICATION NUMBER: US/10/073,865

CURRENT FILING DATE: 2002-02-14

Prior Application removed - See file Wrapper or Palm

NUMBER OF SEQ ID NOS: 154

SEQ ID NO 108

LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 70.6%; Score 72; DB 10; I Best Local Similarity 100.0%; Pred. No. 1.2e-07; Matches 32; Conservative 0; Mismatches 0;
                                                                                                                           LOCATION: (26)...(26)
OTHER INFORMATION: Xaa = Methionine or Threonine
                                                                                                                                                                                                                                          LOCATION: (28)....(28)
OTHER INFORMATION: Xaa = Valine or Phenylalanine
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                              LOCATION: (29)...(29)
OTHER INFORMATION: Xaa = Threonine or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                                                                                                                                                                                                                                                                                                                       : LOCATION: (30)...(30)
; OTHER INFORMATION: Xaa - Cysteine ro Tyrosine US-09-737-178-36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RCLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                                                     LOCATION: (23)...(23)
OTHER INFORMATION: Xaa = Leucine or Proline
NAME/KEY: VARIANT
                   LOCATION: (21)...(21)
OTHER INFORMATION: Xaa - Alanine or Valine
                                                                                                                                                                                  LOCATION: (27)...(27)
OTHER INFORMATION: Xaa = Serine or Leucine
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 94, Application US/09764881; Publication No. US20030125246A9; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
LOCATION: (89)
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Best Local Similarity
                                                        NAME/KEY: VARIANT
                                                                                                                                                                  NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                     NAME/KEY: VARIANT LOCATION: (30)...
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US-09-764-881-94
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. LOCATION: (92)
. OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-881-94
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CACATION: (89)
OTHER THORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-853-659
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FILE REFERENCE: PT207
CURRENT APPLICATION NUMBER: US/09/764,881
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 192
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 94
LENGTH: 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 939 SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 8.2;
2; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PUZON
CURRENT APPLICATION NUMBER: US/09/764,853
CURRENT FILING DATE: 2001-01-17
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Patent No. US20020090673A1
GENERAL INFORMATION
THEORY TROSEN et al.
TITLE OF INVERMION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PIZO1
CURRENT APPLICATION NUMBER: US/09/764,898
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Pred. No. 8.2;
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; Patent No. US20020090672A1
; GENERAL INFORMATION:
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                                                                                                                                               Pred. No. 2.1e+02;
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Pred. No..2.1e+02;
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Pred. No. 2.1e+02;
2; Mismatches 3
                                                                                                                                       Score 35; DB 9;
                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INCRMATION:
APPLICANT: Tania Tamsin Testa
TITLE OF INVENTION:
FILE REFERENCE: GP-3025
CURRENT APPLICATION NUMBER: US/09/788,711A
CURRENT FILING DATE: 2001-02-20
PRIOR FILING DATE: 2000-02-19
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASEEQ for Windows Version 3.0
                                                                                                                                                                            2; Mismatches
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APPLICANT: Tania Tamsin Testa
TITLE OF INVENTYON: NOVEL COMPOUNDS
FILE REFERENCE: GP-30225
CURRENT APPLICATION NUMBER: US/09/788,711A
CURRENT FILING DATE: 2001-02-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 4 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 2001-02-20 PRIOR APPLICATION NUMBER: 0004196.2 PRIOR FILING DATE: 2000-02-19
                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/09788711A Patent No. US20020058328A1
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54.5%;
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54.5%;
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54.5%;
     SOFTWARE: PatentIn version 3.1
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1242 RCVSVLRFDSS 1252
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1242 RCVSVLRFDSS 1252
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Matches 6; Conservative
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Matches 6; Conservative
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ORGANISM: HOMO SAPIENS
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                                                                               ; ORGANISM: Homo sapiens US-10-225-567A-524
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Best Local Similarity
Matches 6; Conserv
                       SEQ ID NO 524
LENGTH: 2923
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LENGTH: 2956
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US-09-788-711A-4
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US-09-788-711A-2
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                                                               TYPE: PRT
                                                                                                                                         Query Match
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APPLICANT: Brown, Joseph P.
APPLICANT: Brown, Joseph P.
APPLICANT: Brumer, Glenna C.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
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                                                                                                                                                                                                                OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09916849A
Bublication No. US20030086934A1
GENERAL INFORMATION:
APPLICANT: Bostein, et al.
TITLE OF INVENTION: Basal Markers in Breast Cancer and Related Reagents
TITLE OF INVENTION: USES Thereof
FILE REPERENCE: 2002850-0024
CURRENT APPLICATION NUMBER: US/09/916,849A
CURRENT FILING DATE: 2010-07-26
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 311
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 286
LENGTH: 96
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                                                                                                                                                                                                                                                                                                                             Score 35; DB 10; Length 96; Pred. No. 8.2;
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Pred. No. 2.1e+02;
2; Mismatches 3; Indels
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PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
                                                                                                                                                                                                                                                                                                                             34.3%;
54.5%;
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54.58;
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Best Local Similarity 54.5
Matches 6; Conservative
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Best Local Similarity 54.5
Matches 6; Conservative
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                                                                                                                   TYPE: PRT
ORGANISM: Homo sapiens
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US-10-225-567A-524
                                                                                                                                                                                                                              NAME/KEY: SITE
LOCATION: (92)
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LENGTH: 2923
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                                                                                                                                                                                        LOCATION:
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Gaps
                            Sequence 996, Application US/09764864
Fatent No. US20020132733A1
GENERAL INFORMATION:
TITLE OF INVENTYON: Wolleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ23
FILE REFERENCE: PTZ23
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 996
LENGTH: 359
TYPE: PRT
TYPE: PRT
TYPE: PRT
CORGANISM: Homo sapiens
US-09-764-864-996
                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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RESULT 15
US-09-764-864-996
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Search completed: July 16, 2003, 18:08:35 Job time: 6.2344 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 16, 2003, 17:50:14; Search time 3.7774 Seconds (without alignments) 814.396 Million cell updates/sec Run on:

US-09-853-079-36 102 1 RCLSIXRFXXSXXFIXIXXXMXFFXXXXXFL 32 Title: Perfect score:

Scoring table:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283224 seqs, 96134422 residues

Searched:

283224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	peroxiredoxin-like	flagellar biosynth	hypothetical prote		S	T-cell surface qly	hypothetical prote	>	hypothetical prote			hypothetical prote		hypothetical prote		delayed rectifier	hypothetical prote	conserved hypothet	hypothetical prote	probable membrane	G protein-coupled	hypothetical prote		_		_	σ	ubiquitin-like pro	ubiquitin - Orgyia
SUMMARIES	ID	T47553	G71290	T20554	T20896	H83754	HLHUR3	G86725	T37806	T33304	T20668	C71675	D89865	E58931	H86832	T14119	T34417	T22209	A98058	S75501	H97143	B45680	T04664	T20174	T23991	T22175	H84469	T36383	T10294	JQ2029
	DB	7	7	~	7	~	П	7	7	~	~	~	~	7													N	~	~	~
	Query Match Length	234	376	208	176	106	335	393	513	670	312	297	373	492	512	3034	528	194	226	264	317	361	310	517	558	617	977	1010	66	93
ø	Query Match	35.3	35.3	34.3	34.3	33.3	32.4	32.4	32.4	32.4	31.9	31.4	31.4	31.4	31.4	31.4	30.9	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	30.4	29.4	29.4
	Score		36		35	34	33	33		m	32.5	32	32	32	32	3	31.5	31	31	31	31	31	31	31	31	31	31	31	30	30
	Result No.		7	m	4	5	9	7	80	თ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

hypothetical prote ribosomal protein	hypothetical prote conserved hypothet	hypothetical prote prophage pi3 prote	hypothetical prote hypothetical prote	hypothetical prote 3',5'-cyclic-nucle	protein C18B10.8 { probable presenili	hypothetical prote probable membrane	hypothetical prote hypothetical prote
S59333 S53852	T16518 G82403	G97831 H86803	T19373 T17764	T20648 A40602	H89102 A84702	S11961 D95947	T18782 T21184
4 2	7 7	0 0	7 7	0.0	77	7 7	7 7
112	217	266	304	327	364	411	523 532
29.4	29.4	29.4	29.4	29.4	29.4	29.4	29.4
30	30	30	30	30	30	30	30
30	32 33	34 35	36	8 6 8 8	40 41	42 43	44

ALIGNMENTS

	RESULT 1 T4753 percoxin-like protein - Arabidopsis thaliana percoxicadoxin-like protein - Arabidopsis thaliana N.Alternate names: protein F8J2.130 C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 C; Accession: T4753 R; Nyakatura, G.; Fartmann, B.; Dauner, D.; Sterr, W.; Holland, R.; Weichselgartner, Mayer, K.F.X. submitted to the Protein Sequence Database, April 2000 A; Reference number: Z24458 A; Accession: T4753 A; Status; preliminary	.ana .ss) 2000 #text_change 20-Apr-2000 .rr, W.; Holland, R.; Weichselgartner, .ril 2000
<u></u>	A; Wolecule type: DNA A; Residues: 1-234 < NYA> A; Cross references: EMBL:AL132969 A; Experimental source: cultivar Columbia; BAC clone F8J2 C; Genetics: A; Map position: 3 A; Note: F8J2.130 Query Match Best Local Similarity 43.8%; Pred. No. 3.1; Matches 7; Conservative 2; Mismatches 7; Indels Oy 3 LSIXRFXXSXXTFIXI 18 Db 5 LSVSRFMSSSATVISV 20	clone F8J2 B 2; Length 234; 1; 7; Indels 0; Gaps 0;

R.; G T.; ⊈

Figgellar biosynthetic protein flhB homolog TP0715 - syphilis spirochete C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C; Accession: G71290; Pc4115
R; Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, R rison, J.; Rhalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, T they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.
Science 281, 375-388, 1998
A; Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete. A; Accession: G71290
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA

A; Residues: 1-376 CCOL>
A; Cross-references: GB:AE001244; GB:AE000520; NID:g3323005; PIDN:AAC65681.1; PID:g332
A; Cross-references: GB:AE001244; GB:AE000520; NID:g3323005; PIDN:AAC65681.1; PID:g332
B; Exacham, J.M.; Frye, J.G.; Stamm, L.V.
Gene 166, 57-64, 1995
A; Title: Identification and sequences of the Treponema pallidum flim', flir, flip, fl
A; Reference number: PC4114; MUID:96105201; PMID:8529894

Gaps

; 0

14; Indels

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HERURS

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T-cell surface glycoprotein CDId precursor - human

N;Alternate names: T-cell surface glycoprotein CDI.R3; thymocyte differentiation anti
C;Species: Homo sapiens (man)
C;Species: Josep-1991 #sequence_revision 30-Sep-1991 #text_change 21-Jul-2000
C;Accession: S07715; A32217; I79469; A30599
R;Calabi, F.; Jarvis, J.M.; Martin, L.; Milstein, C.
Eur: J. Immunol. 19, 285-2292, 1989
A;Title: Two classes of CDI genes
A;Reference number: A30599; MUID:89196496; PMID:2467814
A;Residues: 1-335 cCAL>
A;Residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mucification resistance protein BH0840 [imported] - Bacillus halodurans (strain C-125) C; Species: Bacillus halodurans C; Species: Bacillus halodurans C; Species: Bacillus halodurans C; Species: Bacillus halodurans C; Species: Older C 2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C; Accession: H83754 R; Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; H Nucleic Acids Res. 28, 4317-4331, 2000 A; Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans a A; Reference number: A83550; MUID:20512582; PMID:11058132 A; Status: preliminary A; Molecule type: DNA A; Residues: 1-106 <STO> A; Residues: 
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A;Cross-references: GB:J04142; NID:g619799; PIDN:AAA59673.1; PID:g619800
R;Martin, L.H.; Calabi, F.; Milstein, C.
Proc. Natl. Acad. Sci. U.S.A. 83, 9134-9158, 1986
A;Title: Isolation of CDI genes: a family of major histocompatibility complex-related A;Reference number: 159088; MUID:87067468; PMID:3097645
                                                                A;Gene: CESP:F14F11.1
A;Map position: 2
A;Introns: 67/1; 93/3; 129/3; 169/3; 201/1; 248/3; 291/1; 325/3; 372/2; 440/3; 499/2;
                                                                                                                                                                                                                                          DB 2; Length 776;
14;
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Pred. No. 4
                                                                                                                                                                                                                                               Score 35;
Pred. No.
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Best Local Similarity 42.1%;
Matches 8; Conservative 1
                                                                                                                                                                                                                                               Query Match
Best Local Similarity 33.3 Matches 8; Conservative
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                           C; Genetics:
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A;Accession: PC4115
A;Molecule type: DNA
A;Residues: 1-312 <HAR>
A;Residues: 1-312 <HAR>
A;Cross-references: GB:U36839; GB:U26453; NID:g1216381
C;Comment: This protein is a member of a gene complex involved in the biogenesis and assexport of flagellar protein or virulence factor.
                                                                                                                                                                                                                                                                                                                         A;Gene: flhB; TP0715
C;Superfamily: flagellar biosynthetic protein flhB; flhB carboxyl-terminal homology
C;Keywords: inner membrane
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C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T20896
R;Lightning, J.
Submitted to the EMBL Data Library, October 1995
A;Reference number: Z19342
A;Reference number: Z19342
A;Reference type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-776 <WILL>
A;Cross-references: EMBL: Z54307; PIDN: CAA91092.1; GSPDB: GN00020; CESP: F14F11.1
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A;Cross-references: EMBL:271179; PIDN:CAA94889.1; GSPDB:GN00023; CESP:F07D3.2
A;Experimental source: clone F07D3
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A;Molecule type: DNA
A;Residues: 1-208 GW12>
A;Cross-references: EMBL:Z70755; PIDN:CAA94786.1; GSPDB:GN00023; CESP:F07D3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein F07D3.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20554; T23359
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A; Reference number: 219291
A; Accession: T2054
A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: DNA
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A; Reference number: 219731
A; Accession: T23359
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Best Local Similarity 25.8%;
Matches 8; Conservative
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'-has 6; Conserv?
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10; Indels

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A;Introns: 71/1
C;Superfamily: osmotic growth protein 1; 3-oxosteroid 1-dehydrogenase homology; fumar
E;40-330/Domain: fumarate reductase flavoprotein homology <FRF>
E;384-487/Domain: 3-oxosteroid 1-dehydrogenase homology <OXD>
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A;Introns: 30/2; 70/3; 131/3; 181/3; 275/2; 382/2; 430/2; 455/2; 508/3; 545/1; 575/2
C;Superfamily: Caenorhabditis elegans hypothetical protein R01B10.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-670 <LAN>
A; Cross-references: EMBL: AF068718; PIDN: AAC17769.1; GSPDB: GN00023; CESP: R01B10.5
A; Experimental source: strain Bristol N2; clone R01B10
C; Genetics:
A; Gene: CESP: R01B10.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein R01B10.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 21-Jan-2000
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C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 02-Sep-2000
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A;Introns: 11/3; 143/1; 198/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F32H5.6
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Pred. No. 35;
); Mismatches 9; Indels
                                                                                                                                                                                                                                                 Length 513;
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A;Accession: T33304
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein F09F3.7 - Caenorhabditis elegans
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                                                                                                                                                                                                                                               Score 33; DB 2;
Pred. No. 28;
2; Mismatches 1
A; Experimental source: strain 972h-; cosmid c17A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C,Accession: T20668
R;Thomas, K.
submitted to the EMBL Data Library, October 1996
A;Reference number: Z19308
A;Accession: T20668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31.9%; Score 32.5; D
32.3%; Pred. No. 23;
Live 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C, Accession: T33304
R; Langston, Y.; Beck, C.
submitted to the EMBL Data Library, May 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32.4%; Score 33; 35.3%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                               1 RCLSIXRFXXSXXTFIXIXXXMXFF 25
                                                                                                                                                                                                                                                                                                                                                                                                                   2 RCLTIYTWTFRRLPFIPSTNSASFF 26
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                                                                                                                                                                                                                                                    32.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     606 CFSLFTFSGLSSTFLSI
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Best Local Similarity 32.0v
best Similarity 32.0v
conservative
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Best Local Similarity 32.3
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                   A; Gene: SPDB:SPAC17A2.05
A; Map position: 1
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les 6; Conserv
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL: 299292; PIDN: CAB16560.1; GSPDB:GN00066; SPDB: SPAC17A2.05
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                                                                                                                                                                                                                                                                                                                                                                             Fig. 2010-202/Domain: alpha-2 < EXZ>
Fig. 203-295/Domain: alpha-3 < EXZ>
Fig. 203-295/Domain: alpha-3 < EXZ>
Fig. 203-295/Domain: alpha-3 < EXZ>
Fig. 202-321/Domain: transmembrane #status predicted < TMM>
Fig. 202-335/Domain: intracellular #status predicted < INT>
Fig. 202-335/Domain: intracellular #status predicted < INT>
Fig. 60,126,181/Binding site: carbohydrate (Asn) (covalent) #status predicted
Fig. 201-184,224-279/Disulfide bonds: #status predicted
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-May-2000
C;Accession: T37806
                                                                                                                              A)Cross references: GDB:118764; OMIM:188410
A)Map position: 1922-1923
A)Introns: 21/1; 110/1; 230/1; 296/1; 329/2
C)Complex: heterodimer with beta-0-microglobulin (see PIR:MGHUB2)
C)Superfamily: class I histocompatibility antigen; immunoglobulin homology C;Keywords: glycoprotein; heterodimer; thymocyte; transmembrane protein F:1-19/Domain: slaganl sequence #status predicted <SIG>F:20-335/Product: T-cell surface glycoprotein CDId #status predicted <MAT>F:20-109/Domain: alpha-1 <EX1>
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                                                      A;Cross-references: GB:M14664; NID:9180047; PIDN:AAA51935.1; PID:9180048
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A;Reference number: 221748
A;Accession: T37806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1; Length 335;
Pred. No. 19;
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A;Molecule type: DNA
A;Residues: 1-513 <oLL>
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0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 ISFERFRASIFLFLSLVLNLLYF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 LSIXREXXSXXTFIXIXXXMXFF 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    32.4%;
26.1%;
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Local Similarity 50.0%;
hes 7; Conservative
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Matches 6; Conserv
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                                                                                                             A:Gene: GDB:CD1D
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hypothetical protein yrbb [imported] - Lactococcus lactis subsp. lactis (strain IL140 C; Species: Lactococcus lactis subsp. lactis C; Species: Lactococcus lactis subsp. lactis C; Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001 C; Accession: H86892 R; Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh Genome Res. 11, 731-753, 2001 A; Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis A; Reference number: A86625; MUID:21235186; PMID:11337471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Species: Mus musculus (house mouse)
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C; Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C; Accession: T14119
R; Hadjantonakis, A.K.; Formstone, C.J.; Little, P.F.R.
submitted to the EMBL Data Library, October 1997
A; Description: The Celsr family of novel evolutionarily conserved seven-pass transmem A; Reference number: Z17881
A; Reference number: Z17881
A; Actaus: preliminary, translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
                                                                                                                                                                                                                       A;Genome: mitochondrion
C;Superfamily: NADH dehydrogenase (ubiquinone) chain 4
C;Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylatio
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C;Keywords: transmembrane protein
F;1.26/Domain: signal sequence #status predicted <SIG>
F;27-3034/Product: seven-pass transmembrane receptor protein #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE005176; PID:g12724677; PIDN:AAK05762.1; GSPDB:GN00146 A;Experimental source: strain IL1403
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                            A; Accession: E58931
A; Status: preliminary
A; Solocule type: DNA
A; Residues: 1-492 < ARN>
A; Cross-references: GB: D89861; NID: g4115781; PIDN: BAA36523.1; PID: g4115785
C; Genetics:
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                                                                                                                                                                                                                                                                                                                               Score 32; DB 2; Length 492;
Pred. No. 44;
4; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 512;
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A; Reference number: A58930; MUID:99030526; PMID:9801318
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Pred. No. 46;
0; Mismatches
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C;Superfamily: hypothetical protein sll0855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               362 ILKYYSGLTTFIPLFAVLLFF 382
                                                                                                                                                                                                                                                                                                                                                                                                                                               5 IXRFXXSXXTFIXIXXXMXFF 25
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57.1%;
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Similarity 28.6%;
6; Conservative
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A; Molecule type: DNA
A; Residues: 1-512 <STO>
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Matches 8; Conserv
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Best Local S
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T14119
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A; Residues: 1-297 <AND>
A; Cross-references: GB:AJ235272; GB:AJ235269; NID:g3861033; PIDN:CAAI5125.1; PID:e134296
A; Experimental source: strain Madrid E
C; Genetics:
A; Gene: RP688
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C.Species: mitochondrion Cyanidioschyzon merolae
C:Date: 01-Feb-1999 #sequence_revision 01-Feb-1999 #text_change 03-Jun-2002
C:Accession: E58931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Ohta, N.; Sato, N.; Kuroiwa, T.
Nucleic Acids Res. 26, 5190-5198, 1998
A;Title: Structure and organization of the mitochondrial genome of the unicellular red
                                                                                                                                                                                                                       hypothetical protein RP688 - Rickettsia prowazekii
C;Species: Rickettsia prowazekii
C;Date: 21.Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C;Accession: C71675
R;Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark, Nature 396, 133-140, 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein [imported] - Staphylococcus aureus (strain N315)
C; Species: Staphylococcus aureus
C; Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C; Accession: D89865
R; Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; (Ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, R.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A; Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
A; Accession: D89865
A; Status: preliminary
A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                  A,Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria. A,Reference number: A71630; MUID:99039499; PMID:9823893
A,Recession: C71675
A,Status: preliminary; nucleic acid sequence not shown; translation not shown
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A:Experimental source: strain N315
C;Genetics:
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35;
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Pred. No. 28;
1; Mismatches
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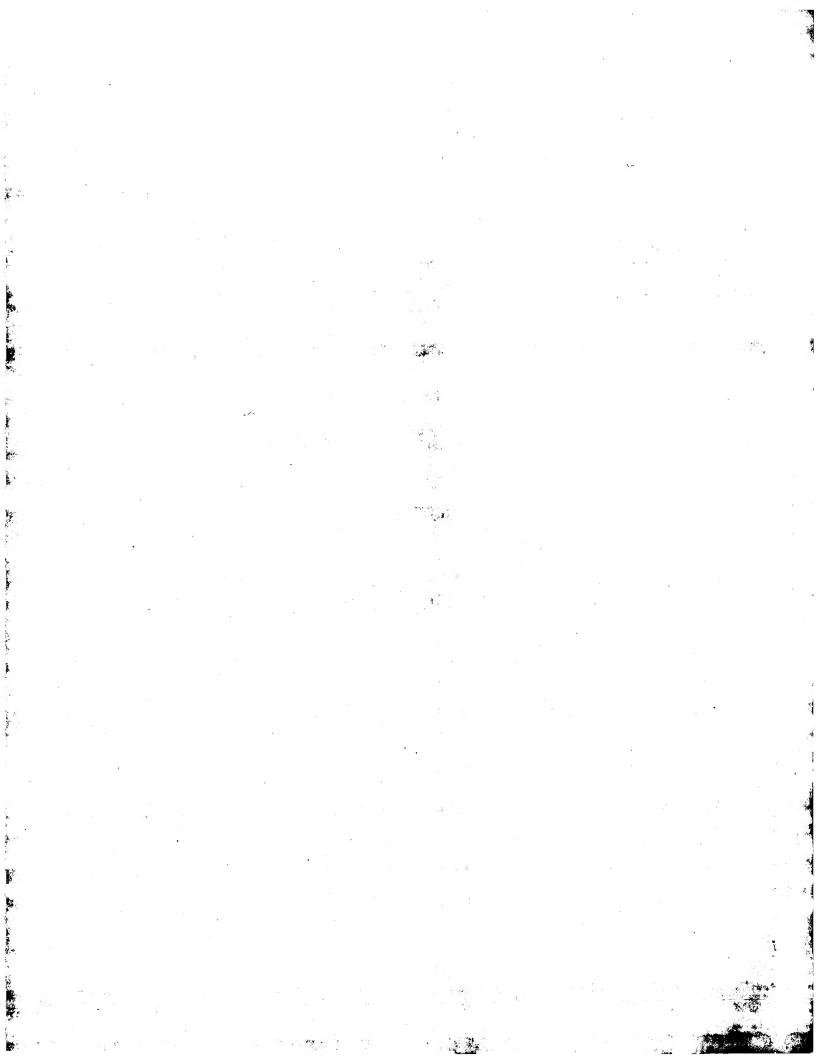
0; Gaps Best Local Similarity 45.5%; Pred. No. 2.1e+02; Matches 5; Conservative 3; Mismatches 3; Indels

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1 RCLSIXRFXXS 11 :|:|: || | 1332 KCVSVLRFDSS 1342

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Search completed: July 16, 2003, 18:09:54 Job time : 6.7774 secs



us-09-853-079-36.rsp

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 16, 2003, 17:37:24 ; Search time 1.8887 Seconds (without alignments) 702.728 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-853-079-36 102 1 RCLSIXRFXXSXXFIXIXXXMXFFXXXXXFL 32

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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SUMMARIES	ID	FLHB_TREPA	CLR2_RAT	CLR2_MOUSE	CLR2_HUMAN	CD1D_HUMAN	Y688_RICPR	CLR1_HUMAN	CLR1_MOUSE	CLR3_MOUSE		CLR3_RAT	EBI2_HUMAN	UBIL_NPVOP	RM05_ACACA	TIM2_CHICK	CPDP_VIBFI	YQE4_CAEEL	X92_TRYBB	YR71_CAEEL	XXNX_CLOTM	KPC1_NEUCR	CO3_ONCMY	YK15_YEAST	RAD4_SCHPO	ABME_RAT	VP43_NPVAC	ADMR_MOUSE	ADMR_RAT	Y294_MYCGE	NU4M_CHOCR	ADRO_SALFO	ICS1_ARATH	YMM1_CAEEL
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34 35	36 37	8 6 8 6 8 7	40	4 4 3	44

ALIGNMENTS

DF 16-OCF-2001 (Rel. DE Flagellar biosynth GN Tribb OR TP0715. OS Treponema pallidum OC Bacteria; Spirocha OX NCBL_TaxID=160; RN [1] RP SEQUENCE FROM N.A. RX SEQUENCE FROM N.A. RX MEDLINE=98332770; RA Fraser C.M., Norri RA Sodergren E., Hard RA Sodergren E., Hard RA Shalak H. Richard	30-MAY-2000 (Rel. 39, Liest sequence update) 16-OCT-2001 (Rel. 34) Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 17-Insert annotation and Insert annotation annotation and Insert annotation a
RA McDonald L., Arti RA Hatch B., Horst R A Venter J.C., RT "Complete genome RT spirochete."; Science 281:375-3 CC '! FUNCTION: REC CC CONSTITUTE THE F CC C CONSTITUTE THE F CC ': SUBCELLULAR I CC ': SIMILARIAL). CC ': SIMILARITY: R	McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S., Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O., Venter J.C.; "Complete genome sequence of Treponema pallidum, the syphilis spirochete."; Science 281:375-388(1998)! FUNCTION: REQUIRED FOR FORMATION OF THE ROD STRUCTURE IN THE BASAL BODY OF THE FLAGELLAR APPARATUS. TOGETHER WITH FLII AND FLIH, MAY CONSTITUTE THE EXPORT APPARATUS OF FLAGELLIN (BY SIMILARITY)! SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane! SIMILARITY: BELONGS TO THE FLHB/HRPN/YSCU/SPAS FAMILY.
	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
CR EMBL; AEO01244; AAC65681.1; DR TIGR; TP0715; EMBL; AEO01244; AAC65681.1; DR TIGR; TP0715; DR PEAM; PF001312; BAC_export_2: 1. DR PRINTS; PR00950; TYPE3IMSPROT. EN FIGREAMS; TIGR00328; flhB; 1. KW Flagella; Transmembrane; Inner FT TRANSMEM 97 117 POF FT TRANSMEM 161 181 POF FT TRANSMEM 161 181 POF FT TRANSMEM 162 222 POF SQUENCE 376 AA; 43039 MW;	BL; AE001244; AAC65681.1; GR; TP0715; TerPro; IPR002065; Bac_export_2: TNTS; PR00950; TYPE31MSPROT. GREAMS; TIGR00328; f1hB; 1. ANSMEM 97 117 POTENTIAL. ANSMEM 161 181 POTENTIAL. ANSMEM 161 181 POTENTIAL. ANSMEM 202 222 POTENTIAL. ANSMEM 202 222 POTENTIAL. ANSMEM 203 222 POTENTIAL. ANSMEM 203 222 POTENTIAL. ANSMEM 204 3339 WW; FEA32E2E8B269540 CRC64;

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PROSITE; PSSUZOO; CLEAR CLOWAIN; 2.
PROSITE; PSSOUZO2; GPE, 1. 6.
PROSITE; PSSOUZO2; EGF_1, 6.
PROSITE; PSOUZO2; EGF_1, 6.
PROSITE; PSOUZO2; EGF_1, 6.
PROSITE; PSOUZO2; EGF_2; 4.
PROSITE; PSOUZO2; GPROTEIN_RECEP_F2_2; FALSE_NEG.
RPOSITE; PSSOUZO; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
RPOSITE; PSSOUZO; G_PROTEIN_RECEP_F2_2; 1.
RPOSITE; PSSOUZO; G_NININ_INPE_EGF; 1.
RPOSITE; PSOUZO48; LAMININ_INPE_EGF; 1.
RPOSITE; PSOUZO48; 1.
RPOSITE; PSOUZO48; LAMININ_INPE_EGF; 1.
RPOSITE; PSOUZO48; LAMININ_INPE_EGF; 1.
RPOSITE; PSOUZO48; 1.
RPOSIT
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CADHERIN 4.
CADHERIN 4.
CAGE-LIKE 1, CALCIUM-BINDING.
EGF-LIKE 2, CALCIUM-BINDING.
EGF-LIKE 3, CALCIUM-BINDING.
LAMININ G-LIKE 1.
EGF-LIKE 4, CALCIUM-BINDING.
LAMININ G-LIKE 2.
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EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
GPS.
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EXTRACELLULAR (POTENTIAL)
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EXTRACELLULAR (POTENTIAL)
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CYTOPLASMIC (POTENTIAL).
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CADHERIN 2.
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BY SIMILAN
                                                                                              SMART: SM00008; HOTMR; 1.
SMART: SM00282; LamG; 2.
PROSITE: PS00010; ASX_HYDROXYL; 2
PROSITE; PS00232; CADHERIN_1; 3.
PROSITE; PS50268; CADHERIN_2; 4.
       SM00112; CA; 3.
SM00179; EGF_CA; 1.
SM00001; EGF_11ke; 6
SM00303; GPS; 1.
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       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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       Gaps
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=Spraque-Dawley; TISSUE-Brain;
STRAIN=Spraque-Dawley; TISSUE-Brain;
STRAIN=Sp88860089; PubMed-9693030;
Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
"Identification of high-molecular-weight proteins with multiple EGF-like motifs by motif-trap screening.";
Genomics 51:27-34(1998).
                                                                                                                                                                                                                   15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
Cadherin EGF LAG seven-pass G-type receptor 2 (Multiple epidermal growth factor-like domains 3) (Fragment).
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    4; Mismatches
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Laminin_EGF.
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EGF_Ca.
EGF_II.
GPCR_secretin.
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HSSP; P00740; IEDM.
InterPro: IPR000152; Asx_hydroxyl..
InterPro: IPR002126; Cadherin.
InterPro; IPR000561; EGF-like.
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Pfam; PF00002; 7tm_2; 1.
Pfam; PF00028; cadherin; 3.
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8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       Rattus norvegicus (Rat).
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2. SUBCELLUING METHON'S INTEGRAL DOIMBLAND.

2. SUBCELLUING LECATION: Integral membrane protein.

2. SUBCELLUING LECATION: Integral membrane protein.

2. CNS, the emerging dorsal root ganglia and cranial ganglia. In the CNS, expression is uniform along the rostrocaudal axis. During gastrulation, it is expressed within the anterior neural ectoderm. At E10, expression is strong in the ventricular zones (WZ) in all sectors of the brain, and lower in the marginal zones (WZ) in all setween E12 and E15, expression is prominant in the brain. It is breadminant. The intensity is higher in all VZ, and lower in differenciating fleids than in VZ, except in the cerebral hemispheres, and to a lesser extent in the tectum and cerebrallum. A weak expression is also observed in the fetal lungs, kidney and epithelia. In the newborn and postnatal stages, expression remains restricted to the VZ as well as in migrating and postmigratory cells throughout the brain.

2. TISSUE SPECIFICTY: Expressed in the CNS and in the eye.

3. SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.

4. SIMILARITY: CONTAINS 1 LAMININ GF-LIKE DOMAINS.

5. SIMILARITY: CONTAINS 1 LAMININ GF-LIKE DOMAINS.

5. SIMILARITY: CONTAINS 1 LAMININ GF-LIKE DOMAINS.

6. SIMILARITY: CONTAINS 1 LAMININ GF-LIKE DOMAINS.
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the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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           signaling during nervous system formation.
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EGF_2; 2.
G_PROTEIN_RECEP_F2_1; F:
G_PROTEIN_RECEP_F2_2; F:
G_PROTEIN_RECEP_F2_3; 1
G_PROTEIN_RECEP_F2_4; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001879; horm_receptor
InterPro; IPR002019; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
InterPro; IPR000203; PKD_cys_rich.
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InterPro; IPR000832; GPCR_secretin.
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InterPro; IPR002126; Cadherin.
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PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00232; CADHERIN_1; 6.
PROSITE; PS50268; CADHERIN_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00008; EGF; 5.
Pfam; PF01825; GPS; 1.
Pfam; PF02793; HRM; 1.
Pfam; PF00054; laminin_G; 2.
PRINTS; PR00205; CANHERIN.
PRINTS; PR00011; EGFLAMININ.
PRINTS; PR000249; GPCRSECRETIN.
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SMART; SM00180; EGF_Lam; 1.
SMART; SM00001; EGF_like; 6.
SMART; SM00303; GPS; 1.
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Pfam; PF00028; cadherin; 9.
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SMART; SM00282; LamG; 2.
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InterPro; I
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PROSITE;
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09R0M0; 0922R4; 099K26;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 2 precursor (Flamingo 1)
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 -!- FUNCTION: Receptor that may have an important role in cell/cell
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Sukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 2144;
BY SIMILARITY.
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HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
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MEDLINE-99418630; PubMed=10490098;
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LAM_G_DOMAIN; 2. receptor; Transmembrane; Glycoprotein; alcium-binding; Laminin EGF-like domain; Repeat; ein; Hydroxlation; Signal. 31 POTENTIAL. 2920 CADHERIN EGF LAG SEVEN-PASS G-TYPE	RECEPTOR 2. EXTRACELLULAR (POTENTIAL). 1 (POTEWIAL).	CYTOPLASMIC (POTENTIAL). 2 (POTENTIAL).	EXTRACELLULAR (POTENTIAL). 3 (POTENTIAL).	CYTOPLASMIC (POTENTIAL). 4 (POTENTIAL).	EXTRACELLULAR (POTENTIAL). 5 (POTENTIAL).	CYTOPLASMIC (POTENTIAL). 6 (POTENTIAL).	EXTRACELLULAR (POTENTIAL). 7 (POTENTIAL).	CYTOPLASMIC (POTENTIAL). CADHERIN 1.	CADHERIN 2.	CADHERIN 4.	CADHERIN 6.	CADHERIN 9.	<u>6</u> Ч	EGF-LIKE 2, CALCIUM-BINDING. EGF-LIKE 3, CALCIUM-BINDING.	LAMININ G-LIKE 1. RGE-IIKE 4 CALCIIM-BINDING	LOST LINE *, CALCION BINDING. LAMININ G-LIKE 2. EGF-IIFF 5. CALCIUM-PINDING	EGF-LIKE 6, CALCIUM-BINDING.	EGF-LIKE 8, CALCIUM-BINDING.	POLY-GLU.	BY SIMILARITY. BY SIMILARITY.	BY SIMILARITY. BY SIMILARITY.	BY SIMILARITY. BY SIMILARITY.	BY SIMILARITY. BY SIMILARITY.	BY SIMILARITY. BY SIMILARITY.	BY SIMILARITY. BY STATIADITY	BY SIMILARITY.		BY SIMILARITY. BY SIMILARITY.			TION (POTENTIA	GLCNAC) (GLCNAC) (N-LINKED (GLCNAC) (POIENTIAL). N-LINKED (GLCNAC) (POTENTIAL). N-TINKED (GLCNAC) (DOPENTIAL).	GLCNAC) (
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FT CARBOHTO 1343 1828 N-LINKED (GLUNC. ) (POTENTIAL).

FT CARBOHTO 1911 3191 3191 3191 N-LINKED (GLUNC. ) (POTENTIAL).

FT CARBOHTO 2446 2244 2244 N-LINKED (GLUNC. ) (POTENTIAL).

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FT CONFLICT 2213 2223 FROM N.A.

FT CONFLICT 2213 2223 FROM N.A.

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CADHERIN 8.

CADHERIN 9.

CADHERIN 9.

EGF-LIKE 1, CALCIUM-BINDING.

EGF-LIKE 2, CALCIUM-BINDING.

LAMININ G-LIKE 1.

EGF-LIKE 5, CALCIUM-BINDING.

LAMININ G-LIKE 1.

EGF-LIKE 6, CALCIUM-BINDING.

EGF-LIKE 7, CALCIUM-BINDING.

EGF-LIKE 7, CALCIUM-BINDING.

EGF-LIKE 8, CALCIUM-BINDING.

EGF-LIKE 10.

EGG-LIKE 
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ID CDID_HUMAN STANDARD;
OF DIS13; Q9Y5M4;
DT 01-APR-1990 (Rel. 14, Created)
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SEQUENCE OF 19-109 FROM N.A., AND VARIANT SER-64.

Han M., Hannick L.I., DiBrino M., Robinson M.A.;

"Polymorphism of human CD1 genes.";

Tissue Antigens 54:122-127(1999).

-I FUNCITION: NOT KNOWN.

-I SUBGELLULAR LOCATION: Type I membrane protein.

-I SUBCELLULAR LOCATION: Type I membrane protein.

-I TISSUE SPECIFICITY: SARRESSED ON CORFICAL THYMCYTES, ON CERTAIN

T-CELL LEUKEMIAS, AND IN VARIOUS OTHER FISSUES.

-I SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY.

-I DATABASE: NAME-PROW; NOTE—CD guide CD1 entry;

WWW-"http://www.ncbi.nlm.nih.gov/prow/cd/cd1.htm".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;
01-APR-1990 (Rel. 14, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
T-cell surface glycoprotein CDld precursor (CDld antigen) (R3G1).
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                                                                                                                                                                                                                            Balk S.P., Bleicher P.A., Terhorst C.; "Isolation and characterization of a cDNA and gene coding for fourth CDI molecule", "Isolation 86:252-256(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR003006; Ig_MHC.
InterPro; IPR003597; Ig_c1.
InterPro; IPR003597; Ig_c1.
SMART: SW00407; Igo; 1.
SMART: SW00407; Igo; 1.
Glycoprotein; Signal; Transmembrane; Immunoglobulin domain;
                                                                                                                                  MEDLINE-89196496; PubMed-2467814;
Calabi F., Jarvis J.W., Martin L., Milstein C.;
"Two classes of CDI genes.";
"Two Inmunol. 19:285-292(1989).
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EMBL, L38815; AAA59672.1; JOINED.
EMBL, L38816; AAA59672.1; JOINED.
EMBL, L38816; AAA59672.1; JOINED.
EMBL, L38818; AAA59672.1; JOINED.
EMBL, L38819; AAA59672.1; JOINED.
EMBL, L38819; AAA59672.1; JOINED.
EMBL, J04142; AAA59673.1; --
                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-89098892; PubMed=2463622;
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                                                      Homo sapiens (Human)
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PIR; A32217; A32217
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Science 290:347-350(2000).
-1- SIMILARITY: STRONG, TO R.PROWAZEKII RP689. SOME TO H.INFLUENZAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=Madrid E;
MEDLINE=99039499; PubMed=9823893;
MEDLINE=99039499; PubMed=9823893;
MAGETSON S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of mitochondria.";
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Ogata H., Audic S., Barbe V., Artiguenave F., Fournier P.-E.
Raoult D., Claverie J.-M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=782;
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TIGRRAMs; TIGR01045; RPB; 1.
Hypothetical protein; Transmembrane; Complete proteome.
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EA041C1C45A5777F CRC64;
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16-OCT-2001 (Rel. 40, Last anno
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                                                                                           37717 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34878 MW;
                                                                                                                                          32.4%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2001 (Rel. 40, Last
Hypothetical protein RP688
                                                                                                                                                                                                                                                                                    29 RCLQISSFANSSWT 42
                                                                                                                                                                                                                                     1 RCLSIXRFXXSXXT 14
                                                                                                                 Ouery Match
Best Local Similarity 50.0.
Tr Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 396:133-140(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
126
181
64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rickettsia prowazekii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62
297 AA;
                                                                                             335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                      RESULT 6
Y688_RICPR
ID Y688_RICPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN RPE1.
                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                              VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                09ZCN5;
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REDLINES-20057165; Pubbmed=10591208;
RA Dunham I. Hunt A.R., Collins B. Bruskiewich R., Beare D.M., Clamp M., Smitk L.J., Almacough R., Almeida J.P., Babbage A.K., Radauley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Radauley C., Bailey J., Barlow K.F., Bates K.N., Beasley O.P., Radauley C., Bulkey S.E., Colline R.E., Connor R., Conroy D., Corby N.R., Coville G.J., Cox A.V., Davis J., Davson E., Conroy D., Corby N.R., Collier R.E., Connor R., Glegg S.M., Fleming K., French L., Garner A.A., Radans K.L., Fey J.M., Fleming K., French L., Garner A.A., Radiller J.G.R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C., Radans R.L., Edyller R., Goward M.E., Grafham D.V., Griffiths M.N.D., Hall C., Radiller J.G.R., Langford C.F., Leversha M.A., Liloyd C., Lloyd C.M., Mathrephi-Mohammadi M., Mathrews L.H., Mccann O.T., Matlik S.H., Langford C.F., Leversha M.A., Liloyd C., Lloyd C.M., Mathrephi-Mohammadi M., Mathrews L.H., Mccann O.T., Matric G., Hearloot R.A., Milles S.H., Mortimore B.J., C.T., Phillips S.H., Plumb R.W., Stewer C.D., Sanlay Y., Rogers J., Shimizu N., Mathrey J., Mclaren S., Wennissy H., Ramsey Y., Rogers J., Shimizu N., Mulliams C., Spragon L., Steward C.A., Sulston J.E., Swann R.M., Williams S.A., Williams S., Rawasaki K., Sasaki T., Sacker C.E., Sahra H.K., Stwoe C.D., Sanlaley S., Smith M. L., Soderlund C., Spragon L., Steward C.A., Sulston J.E., Swann S., Rawasaki K., Sasaki T., Asakawa S., Kudoh J., Ramsey H., Milliams S., Rawasaki K., Sasaki T., Asakawa S., Kudoh J., Ramsey J., Milley D.L., Raming J., Milliams S., Rawasaki K., Sasaki T., Asakawa S., Kudoh J., Shibuya K., Noshibuya K., Wohldmann A., Shibuya K., Woshizaki Y., Aoki N., Milley J., Lewis S., Lin S., P., Loh P., Malaj E., Wulley J., Milliamson A., Ramsey W., Milliamson B., Band M., Songer D., Band M., Shinger C., Mang Y., Wang Y., Wohl C.C., Morrow B.E., Edelmann L., Ramaled B.S., Shaikh T., Kurahashi H., Saitta S., Baudar M., Shongu H., Shonson D., Bemis G., Bentley D., Pergers D., Lohnson D., Bemis G., Bentley D., Perger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Receptor that may have an important role in cell/cell
                         CLR1_HUMAN STANDARD; PRT; 3014 AA. 059V526; 09Y526; 09F526; 09F506; 095722; 09BW05; 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Cadherin EGF LAG seven-pass G-type receptor 1 precursor (Flamingo
                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                            Large exons encoding multiple ectodomains are a characteristic
                                                                                                                                                                                                                                                                           feature of protocadherin genes.";
Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'The DNA sequence of human chromosome 22.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 624-3014 FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-20202599; PubMed-10716726;
Wu Q., Maniatis T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 402:489-495(1999).
                                                                                                              homolog 2) (hFmi2).
CELSR1 OR CDHF9 OR FMI2.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Filahun Y., Wright
                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'ISSUE=Kidney;
               CLR1_HUMAN
RESULT
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                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                         produced by alternative splicing.
-: SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
-:- SIMILARITY: CONTAINS 9 CAPHERIN DOMAINS.
-:- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
-:- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAINS.
-:- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
-:- SIMILARITY: CONTAINS 1 GPS DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS00650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
PROSITE; PS01248; LAM_G_DOMAIN; 2.
PROSITE; PS50025; LAM_G_DOMAIN; 2.
PROSITE; PS50025; LAM_G_DOMAIN; 2.
EGF-Like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
Developmental protein; Hydroxylation; Signal; Alternative splicing.
                           SUBCELLULAR LOCATION: Integral membrane protein. ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CADHERIN EGF LAG SEVEN-PASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FALSE_NEG.
FALSE_NEG.
nervous system formation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G_PROTEIN_RECEP_F2_1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTOR 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AL031597; CAB45020.1; ALT_INIT.
EMBL, AL031588; CAB38413.1; -.
EMBL, BC000059; AAH00059.1; -.
Genew, HGNC:1850; CELSRI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hormn_receptor
Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPCR_secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MAKT; SMUUZOZ; LOMU, Z.
PROSITE; PSO0010; ASX_HYDROXXL; 2.
PROSITE; PSO0232; CADHERIN_1; 7.
PROSITE; PSS0268; CADHERIN_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001791; Laminin_G.
InterPro; IPR000203; PKD_cys_rich.
Pfam; PF00002; 7tm_2; 1.
Pfam; PF00028; cadherin; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Asx_hydroxyl Cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF231024; AAF61930.1; -. EMBL; AL021392; CAB50707.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00054; laminin_G; 1.
PRINTS; PR00205; CADHERIN.
PRINTS; PR00011; EGFLAMININ.
PRINTS; PR00249; GPCRSECRETIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00249; GPCRSECRETIN SMART; SM00112; CA; 9.
SMART; SM00180; EGF_LAM; 1.
SMART; SM00001; EGF_like; 6.
SMART; SM00303; GPS; 1.
SMART; SM00008; HOTMR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3014
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interPro; IPR002049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PF01825; GPS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00022; E
PROSITE; PS50221; G
PROSITE; PS50221; G
PROSITE; PS00649; G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P00749; 1URK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2491
2502
2523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MIM; 604523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RANSMEM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kidney and epithelia.
--- TISSUE SPECIFICITY: Expressed in the brain, where it is localized principally in the ependymal cell layer, choroid plexus and the area postrema. Also found in spinal chord and in the eye.
--- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
--- SIMILARITY: CONTAINS 9 CADHERIN DOWAINS.
--- SIMILARITY: CONTAINS 2 LAMININ G-LIKE DOWAINS.
--- SIMILARITY: CONTAINS 1 LAMININ GF-LIKE DOMAINS.
--- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                 Tissir F., De-Backer O., Goffinet A.M., Lambert de Rouvroit C.A.; "Developmental expression profiles of Celsr (Flamingo) genes in the mouse.";
                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                  Hadjantonakis A.-K., Formstone C.J., Little P.F.R.; "mcelsr1 is an evolutionarily conserved seven-pass transmembrane receptor and is expressed during mouse embryonic development."; Mech. Dev. 78:91-95(1998).
                                                                                                                                                                   STRAIN=C57BL/6; TISSUE=Brain; MEDLINE=97480720; PubMed=9339365; Hadjantonakis A.-K., Sheward W.J., Harmar A.J., de Galan L., Hoovers J.M. N., Little P.F. R.; "Celsr1, a neural-specific gene encoding an unusual seven-pass transmenarae receptor, maps to mouse chromosome 15 and human chromosome 22gter." Genemics 45:97-104(1997).
   Cadherin EGF LAG seven-pass G-type receptor 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hormn_receptor.
Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EGF-like.
GPCR_secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000152; Asx_hydroxyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF031572; AAC68836.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Laminin_G.
                                                                                                                                                                                                                                                                                                                         Mech. Dev. 112:157-160(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1100883; Celsr1.
HSSP; P00749; 1URK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR002126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000561;
InterPro; IPR000832;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR001879;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001791;
                                                                                                                                                                                                                                                                      DEVELOPMENTAL STAGE.
                                                                              SEQUENCE FROM N.A.
                                                                                                                                                          TISSUE SPECIFICITY
                                                         NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                PubMed=11850187;
                                                                                          PubMed=9858697;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3014;
                                                                                                                               CADHERIN 2.
CADHERIN 4.
CADHERIN 5.
CADHERIN 5.
CADHERIN 7.
CADHERIN 7.
CADHERIN 9.
CADHERIN 9.
EGF-LIKE 1, CALCIUM-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; L...
1.38+02;
3; Indels
                                                                                                                                                                                                                                                                 LAMININ G-LIKE 2.

EGF-LIKE 5, CALCIUM-BINDING.

EGF-LIKE 6, CALCIUM-BINDING.

EGF-LIKE 7, CALCIUM-BINDING.

EGF-LIKE 8, CALCIUM-BINDING.
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
5 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
6 (POTENTIAL).
EXTRACELLUIAR (POTENTIAL).
7 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                    CALCIUM-BINDING
                                                                                                                                                                                                                                                          CALCIUM-BINDING
                                                                                                                                                                                                                                             LAMININ G-LIKE 1.
EGF-LIKE 4, CALCI
                                                                                                                                                                                                                                                                                                                        LAMININ EGF-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 41, Created)
(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY.
SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32; DB
Pred. No. 1.3e
                                                                                                                                                                                                                                                                                                                                                           SIMILARITY SIMILARITY
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                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY
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45.5%;
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1317 KCVSVLRFDSS 1327
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Best Local Similarity
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Gaps
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0912.10; 09ESD0;
15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin EGF LAG seven-pass G-type receptor 3 precursor.
CELSR3
Was musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
10090;
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HYDROXYLATION (POTENTIAL).
HYDROXYLATION (POTENTIAL).
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1332 KCVSVLRFDSS 1342
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Best Local Similarity 45.5
Matches 5; Conservative
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CLR3_MOUSE
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CADHERIN 7.
CADHERIN 8.
CADHERIN 9.
EGF-LIKE 1, CALCIUM-BINDING.
EGF-LIKE 2, CALCIUM-BINDING.
LAMININ G-LIKE 1.
EGF-LIKE 3.
LAMININ G-LIKE 1.
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EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
LAMININ EGF-LIKE.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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PROSTIE; PSO1248: LANIN_TYPE_EGF; 1.
PROSTIE; PSO1248: LANIN_TYPE_EGF; 1.
PROSTIE; PSO121: GPS; 1.
PROSTIE; PSO6049; GPGOTEIN_RECEP_F2, 1; FALSE_NEG.
PROSTIE; PSO650: G_PROTEIN_RECEP_F2, 2; FALSE_NEG.
PROSTIE; PSO650: G_ROTEIN_RECEP_F2, 1; 1.
PROSTIE; PSO5041; G_ROTEIN_RECEP_F2, 1.
G-protein coupled receptor; Transmembrane; Glycoprotein; G-protein binding; Lamin EGF-like domain; Repeat; Bevelopmental protein; Hydroxylation; Signal.
SIGNAL
                                                                                                                                                 CADHERIN EGF LAG SEVEN-PASS G-TYPE RECEPTOR 3.
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EGF-LIKE 2, CALCIUM-BINDING.
EGF-LIKE 3, CALCIUM-BINDING.
LAMININ G-LIKE 1.
EGF-LIKE 4, CALCIUM-BINDING.
LAMININ G-LIKE 2.
EGF-LIKE 5, CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
EGF-LIKE 9, CALCIUM-BINDING.
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EXTRACELLULAR (POTENTIAL).
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              EGF_1; 5.
EGF_2; 4.
LAMININ_TYPE_EGF;
    CADHERIN_2;
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                Tissir F., De-Backer O., Goffinet A.M., Lambert de Rouvroit C.A., "Developmental expression profiles of Celsr (Flamingo) genes in the
                                                                                                        Formstone C.J., Little P.F.R.; The flamingo-related mouse Celsr family (Celsr1-3) genes exhibit distinct patterns of expression during embryonic development."; Mech. Dev. 109:91-94(2001).
                                                                                    SEQUENCE OF 2574-3046 FROM N.A., AND DEVELOPMENTAL STAGE.
PubMed=11677057;
SEQUENCE FROM N.A., AND DEVELOPMENTAL STAGES.
STRAIN-C57BL/6;
PubMed-11850187;
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EMBL; AF188752; AAG17057.1; ALT_FRAME
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IPR000832; GPCR_secretin.
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IPR002126; Cadherin.
IPR000561; EGF-like.
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InterPro; IPR000203; PKD_cys_rich.
Pfam; PF00002; 7tm_2; 1.
                                                                Mech. Dev. 112:157-160(2002)
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Pfam; PF00008; EGF; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1858236; Celsr3.
                                                                                                                                                            TISSUE SPECIFICITY.
PubMed=10790539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF02793;
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InterPro;
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PR00011; EGFLAMININ.
PR00249; GPCRSECRETIN.
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SMART; SM00180; EGF_Lam; 1.
SMART; SM00001; EGF_like; 6.
SMART; SM00303; GPS; 1.
SMART; SM0008; HOTMR; 1.
SMART; SM00282; LamG; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PR00205; CADHERIN.
                                                                                                                                                                          Genew; HGNC: 3230; CELSR3.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: Receptor that may have an important role in cell/cell signaling during nervous system formation.
-i- SUBCELLULAR LOCATION: Integral membrane protein.
-i- SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
-i- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
-i- SIMILARITY: CONTAINS 2 EGF-LIKE DOMAINS.
-i- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O., indentification of high-molecular-weight proteins with multiple EGF-like motifs by motif-trap screening.", Genomics 51:27-34(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLR3_HUMAN STANDARD; PRT; 3312 AA.

GONYO7: 075092;
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Created)
16-JUN-2002 (Rel. 41, Created)
16-JUN-2002 (Rel. 41, Last annotation update)
17-JUN-2002 (Rel. 41, Last annotation update)
18-JUN-2002 (Rel. 41, Last annotation update)
18-J
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                         (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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(POTENTIAL).
(POTENTIAL).
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MEDLINE-20202599; PubMed-10716726;
Wu O., Manhatis T.:
"Large exons encoding multiple ectodomains are a characteristic
                                                                             (POTENTIAL) (POTENTIAL)
                                                                                                                                                                                      (POTENTIAL)
                                                                                                                                                                                                                                                                 (POTENTIAL)
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Pred. No. 1.4e+02;
3; Mismatches 3; Indels
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MW; A6B18F2DF7F4DEB6 CRC64;
                                                             HYDROXYLATION (POTENTIAL)
                                                                     N-LINKED (GLCNAC...) (F
N-LINKED (GLCNAC...) (I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   feature of protocadherin genes.";
Proc. Natl. Acad. Sci. U.S.A. 97:3124-3129(2000).
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N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC.
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R -> P (IN REF. 2
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MEDLINE-98360089; PubMed-9693030;
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45.5%;
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Best Local Similarity 45.5-
Best Local Similarity 45.5-
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1380 KCVSVLRFDSS 1390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-protein coupled receptor; Transmembrane; Glycoprotein;
EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat;
Developmental protein; Hydroxylation; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL.
CADHERIN EGF LAG SEVEN-PASS G-TYPE
RECEPTOR 3.
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CYTOPLASMIC (POTENTIAL).
2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
3 (POTENTIAL).
CYTOPLASMIC (POTENTIAL).
4 (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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FALSE_NEG.
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PROSITE: PS01186; EGF_2; 4.
PROSITE: PS01286; EGF_2; 4.
PROSITE: PS01286; EGF_1; FAI
PROSITE: PS00649; G_PROTEIN_RECEP_F2_1; FAI
PROSITE: PS50227; G_PROTEIN_RECEP_F2_2; FAI
PROSITE: PS50221; G_PROTEIN_RECEP_F2_4; 1.
PROSITE: PS50261; G_PROTEIN_RECEP_F2_4; 1.
PROSITE: PS01248; LAM_C_DOMAIN; 2.
PROSITE: PS01248; LAM_C_DOMAIN; 2.
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                                                                                                                                                                                                                                                                                                                                   Interpro; 198002126; Cadherin.
Interpro; 198000561; BGF-11ke.
Interpro; 198000142; BGF_2.
Interpro; 198001891; BGF_Ca.
Interpro; 198001893; Horm_receptor.
Interpro; 198002893; Horm_receptor.
Interpro; 198002049; Laminin_BGF.
Interpro; 198001791; Laminin_GF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001791; Laminin_G.
InterPro; IPR001791; Laminin_G.
InterPro; IPR00203; PKD_cys_rich.
Pfam; PF000028; cadherin; 9.
Pfam; PF00008; EGF; 6.
Pfam; PF001825; GPS; 1.
Pfam; PF001793; HRM; 1.
Pfam; PF00054; laminin_G; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00282; LamG; 2.
PROSITE; PS00010; ASX_HYRBXYL; 1.
PROSITE; PS00232; CADHERIN_1; 7.
PROSITE; PS50268; CADHERIN_2; 8.
                                                                                                                                                                                                                                                                                    MIM; 604264; -.
InterPro; IPR000152; Asx_hydroxyl
InterPro; IPR002126; Cadherin.
InterPro; IPR000561; EGF-1ike.
                                                                                                                                                                                              EMBL; AF231023; AAF61929.1; -. EMBL; AB011536; BAA32464.1; -.
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                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                         brain stem.

-! SIMILARITY: BELONGS TO FAMILY 2 OF G-PROTEIN COUPLED RECEPTORS.
-!- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.
-!- SIMILARITY: CONTAINS 8 EGF-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ G-LIKE DOMAINS.
-!- SIMILARITY: CONTAINS 1 LAMININ EGF-LIKE DOMAIN.
-!- SIMILARITY: CONTAINS 1 GPS DOMAIN.
                                       15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cadherin.EGF LAG seven-pass G-type receptor 3 precursor (Multiple epidermal growth factor-like domains 2).
  3313 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; PROJATO, DESCRIPTION HSSP; PROJATO, DESCRIPTION HSSP; PROJATO, DESCRIPTION HEAPTO, IPROMO1225, Cacherin.
InterPro; IPROMO1261; EGF-2.
InterPro; IPROMO1881; EGF-2.
InterPro; IPROMO1891; EGF-2.
InterPro; IPROMO1892; GPR_Secretin.
InterPro; IPROMO1892; Horm_receptor.
InterPro; IPROMO1891; Laminin_EGF.
InterPro; IPROMO2049; Laminin_EGF.
InterPro; IPROMO2049; Laminin_EGF.
InterPro; IPROMO203; PRO_CYS_rich.
Pfam; PFOMO08; EGF, 6.
Pfam; PFOMO08; EGF, 6.
Pfam; PFOMO08; EGF, 6.
Pfam; PFOMO08; EGF, 6.
Pfam; PFOMO08; IRW; 1.
Pfam; PFOMO084; Laminin_G; 1.
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SMART; SM00180; EGF_Lam; 1.
SMART; SM00001; EGF_Like; 6.
SMART; SM00001; EGF_Like; 6.
SMART; SM00203; GPS; 1.
SMART; SM00282; LamG; 2.
SMART; SM00282; LamG; 2.
PROSITE; PS00010; ASX_HYDROXYL; 1.
PROSITE; PS00232; CADHERIN_L; 7.
PROSITE; PS50268; CADHERIN_L; 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00122; EGF_1; 6.
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS50221; GPS; 1.
PROSITE; PS50025; LAM_G_DOMAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AB011528; BAA32459.1; -. HSSP; P00740; 1EDM.
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PROSITE; PS00022;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 NCBI_TaxID=10116;
    ö
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CADHERIN 6.
CADHERIN 6.
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CADHERIN 9.
CADHERIN 9.
CADHERIN 9.
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CADHERIN 9.
EGF-LIKE 1, CALCIUM-BINDING.
EGF-LIKE 2, CALCIUM-BINDING.
LAMININ G-LIKE 1.
EGF-LIKE 6.
CALCIUM-BINDING.
EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8.
CALCIUM-BINDING.
EGF-LIKE 9.
CALCIUM-BINDING.
EGF-LIKE 1.
EGF-LIKE
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Pred. No. 1.4e+02;
3; Mismatches 3; Indels
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MW; BEC208703651A4A5 CRC64;
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KCVSVLRFDSS 1399
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kieff E.;
"Epstein-Barr virus-induced genes: first lymphocyte-specific G
protein-coupled peptide receptors.";
J. Virol. 67:2209-2220(1993)
-!- FUNCTION: ORPHAN RECEPTOR. PROBABLE MEDIATOR OF EBV EFFECTS ON B
IVAMPHOCYTES OR OF NORMAL LYMPHOCYTE FUNCTIONS.
-!- INSUE SPECIFICITY: B-LYMPHOCYTE CELL LINES.
-!- INDUCTION: BY EBV.
-!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
-!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-5 IS THE INITIATOR.
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Catarrhini; Hominidae; Homo.
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MEDLINE-93188173; Pubmed-8383238;
Birkenbach M.P., Josefsen K., Yalamanchili R.R., Lenoir G.M.,
                                                                                                                                                                                    Length 3313;
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Pfam; PF00001; 7tm 1; 1.
PRINTS; PR00237; GPCRHODOPSN.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_1; 1.
PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
OPROTEIN coupled receptor; Transmembrane; Glycoprotein.
DOMAIN 32 57 1 (POTENTIAL).
                                                                                                                                                            MW; B11DA09517288764 CRC64;
                                                                                                                                                                          Score 32; DB 1; Le
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                     01-ocT-1993 (Rel. 27, Created)
01-ocT-1993 (Rel. 27, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
EBV-induced G protein-coupled receptor 2 (EBI2)
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Mammalia; Eutheria; Primates;
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MIM; 605741; -.
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tes 5; Conserv
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         PROSITE; PSO0650; G_PROTEIN_RECEP_F2_2; FALSE_NEG.
PROSITE; PS50221; G_RROTEIN_RECEP_F2_3; 1.
PROSITE; PS50261; G_RROTEIN_RECEP_F2_4; 1.
PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
PROSITE; PS01248; LAMININ_TYPE_EGF; 1.
EGF101: Coupled receptor; Transmembrane; Glycoprotein; EGF-like domain; Calcium-binding; Laminin EGF-like domain; Repeat; Developmental protein; Hydroxylation; Signal.
                                                                                                  CADHERIN EGF LAG SEVEN-PASS G-TYPE RECEPTOR 3.
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CACIUM-BINDING.
EGF-LIKE 2, CALCIUM-BINDING.
EGF-LIKE 4, CALCIUM-BINDING.
LAMININ G-LIKE 1.
EGF-LIKE 4, CALCIUM-BINDING.
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EGF-LIKE 6, CALCIUM-BINDING.
EGF-LIKE 7, CALCIUM-BINDING.
EGF-LIKE 8, CALCIUM-BINDING.
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PRINTS; PRO0348; UBIQUITIN.
SMART; SM00213; UBQ; 1.
PROSITE; PS00299; UBIQUITIN_1; 1.
PROSITE; PS50053; UBIQUITIN_2; 1.
                                             Nuclear protein; Late protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93286576; PubMed-8389803; Russell R.L.O., Rohrmann G.F.; "Nucleotide sequence of the ubiquitin-39K gene region from the Orgyla pseudotsugata multinucleocapsid nuclear polyhedrosis virus genome."; J. Gen. Virol. 74:1191-1195(1993).
                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-97271300; PubMed=9126251;
Ahrens C.H., Russell R.R., Funk C.J., Evans J., Harwood S.,
Rohrmann G.F.,
"The sequence of the Orgyia pseudotsugata multinucleocapsid nuclear
polyhedrosis virus genome.",
Virology 229:381-399(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i-FUNCTION: UBIQUITIN MAY PLAY A ROLE IN VIRAL LIFE CYCLES, OR IN VIRAL WAYS-HOST INTERACTIONS. IT IS COVALENTLY LINKED TO COAT PROTEIN SUBUNITS OF SEVERAL DIFFERENT PLANT AND ANIMAL VIRUSES.
                                                                                                                                                                                                                 ;
0
                                                                                                                                                                                                                                                                                                                                                                                             Orgyia pseudotsugata multicapsid polyhedrosis virus (OpMNPV).
Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
Nucleopolyhedrovirus.
                                                                                                                                                                                          Score 31; DB 1; Length 361;
                                                                                                                                 CYTOPLASMIC (POTENTIAL). INTERACTION WITH G PROTEINS.
                                                                                                                                                                                                                 1; Indels
                                                                                                              EXTRACELLULAR (POTENTIAL).
          2 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                     4 (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                   B5A2171F34C9C67B CRC64;
 CYTOPLASMIC (POTENTIAL).
                                3 (POTENTIAL). CYTOPLASMIC (POTENTIAL).
                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                    01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Ubiquitin-like protein.
                                                                                                                                                                                                                                                                                                                  93 AA.
                                                                                                 6 (POTENTIAL).
                                                                            5 (POTENTIAL).
                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                    Pred. No. 26;
0; Mismatches
                                                                                                                                                          SIMILARITY
                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D13375; BAA02639.1; -.
EMBL; U75930; AAC59024.1; -.
PIR; J02029; J02029.
HSSP; P02248; 1UBI.
InterPro; IPR000626; Ubiquitin.
Pfam; PF00240; ubiquitin; 1.
                                                                                                                                                                   41224 MW;
                                                                                                                                                                                          30.4%;
                                                                                                                                                                                                   Local Similarity 85.7
nes 6; Conservative
                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                 265
                                                                                                                                                                                                                                                          124 CLSIDRF 130
58
96
106
1128
1159
1169
2193
216
2286
288
313
313
361
AA,
                                                                                                                                                                                                                                     2 CLSIXRF 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=164623;
                                                                                                                                                                                                                                                                                                                UBIL_NPVOP
                                                                                                                                                       DISULFID
SEQUENCE
DOMAIN
TRANSMEM
                               TRANSMEM
DOMAIN
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TRANSMEM
                                                      PRANSMEM
                                                                            PRANSMEM
                                                                                                  TRANSMEM
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                                                                  DOMAIN
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                       DOMAIN
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                                                                                                                                                                                                                                                                                                      UBIL_NPVOP
                                                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

STRAIN=ATCC 30010 / NEFF;

MEDLINE-95147275; PubMed-8444823;

Burger G., Plante I., Lonergan K.M., Gray M.W.;

The mitochondrial DNA of the amoeboid protozoon, Acanthamoeba castellanii: complete sequence, gene content and genome organization."

J. Mol. Biol. 245:522-537(1995).

SUBCELLULAR LOCATION: Mitochondrial.

SIMILARITY: BELONGS TO THE LSP FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                  ;
0
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MULTIUBIQUITIN ADDUCTS.
CONJUGATION TO ACCEPTOR PROTEINS.
681B2A99DE964C99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 177;
                                                                                              DB 1; Length 93,
                                                                                                                                                  · 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    177 AA; 21764 MW; BEA1930DBC375274 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
                                                                                              Score 30; DB 1
Pred. No. 12;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                            177 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          220 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002132; Ribosomal_L5.
Pfam; PF00281; Ribosomal_L5; 1.
PROSITE; PS00358; RIBOSOMAL_L5; FALSE_NEG.
Ribosomal protein; Mitochondrion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Acanthamoebidae; Acanthamoeba.
NCBI_TaxID=5755;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29.4%; Score 30; 37.5%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitochondrial 60S ribosomal protein L5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Acanthamoeba castellanii (Amoeba).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIM2_CHICK STANDARD; 042146; 15-JUL-1998 (Rel. 36, Created)
                       76 76
93 AA; 10427 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 KCLKYNRFENSLILYI 130
                                                                                                 29.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RCLSIXRFXXSXXTFI 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U12386; AAD11844.1; -.
                                                                                                                                                  5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                               |||||: :|
85 RCLSLLQF 92
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Best Local Similarity
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                                                SEQUENCE
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                                                                                                                                                                                                                                                                                                                                           MEDLINE-98122528; PubMed=9462696; MEDLINE-98122528; PubMed=9462696; MEDLINE-98122528; PubMed=9462696; Mimes R.T., Li L.H., Weaver B., Hawkes S., Hahn-Dantona E.A., Quigley J.P.; Cloning, expression, and characterization of chicken tissue inhibitor of metalloproteinase-2 (TIMP-2) in normal and transformed chicken embryo fibroblasts."

J. Cell. Physiol. 174:342-352(1998).

--- FUNCTION: COMPLEXES WITH METALLOPROTEINASES (SUCH AS COLLAGENASES) AND IRREPESSIBLE THEM (BY SIMILARITY).
15-JUL-1998 (Rel. 36, Last sequence update)
16-GCT-2001 (Rel. 40, Last annotation update)
Metalloproteinase inhibitor 2 precursor (TIMP-2) (Tissue inhibitor of
metalloproteinases-2).
                                                                                                                                                        Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Secreted.
-!- PIM: THE ACTIVITY OF TIMP-2 IS DEPENDENT ON THE PRESENCE OF DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29.4%; Score 30; DB 1; Length 220; ilarity 63.6%; Pred. No. 27; Conservative 0; Mismatches 4; Indels
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61BDAC760B752E53 CRC64;
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Metalloprotease inhibitor; Signal.
SIGNAL 1 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF004664; AAB69168.1; -. HSSP; P16035; 2TMP. InterPro; IPR001820; TIMP. Pfam; PF00965; TIMP; 1. SMART; SM00206; TIMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity (
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                                                                                                                                                                                                                                                                               NCBI_TaxID=9031;
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SEQUENCE
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Search completed: July 16, 2003, 17:47:26 Job time : 3.8887 secs

oy Db

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 16, 2003, 17:37:48; Search time 7.77066 Seconds (without alignments) 848.513 Million cell updates/sec Run on:

US-09-853-079-36 102 1 RCLSIXRFXXSXXFIXIXXXMXFFXXXXXFL 32 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SPTREMBL_21:*

sp_archea:*
sp_bacteria:*
sp_fungi:*
sp_human:*
sp_human:*
sp_nammal:*
sp_mammal:*
sp_mnc:*
sp_pnage:*
sp_pnage:*
sp_pnage:*
sp_pnage:*
sp_pnage:* sp_virus:*
sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:* Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Description	Q9nim3 babesia mic	Q949u7 arabidopsis	Q91f96 arabidopsis	Q56337 treponema p	Q19464 caenorhabdi	Q9qyp2 rattus norv	Q92566 homo sapien	Q9r0m0 mus musculu	Q9hcu4 homo sapien	Q9kel2 bacillus ha	Q96cl0 homo sapien	Q96ux9 hebeloma cy	Q9vwq4 drosophila	Q9chc5 lactococcus	Q9vwk3 drosophila	013755 schizosacch
CHIMMING			B ID	5 Q9NIM3	10 094907	10 Q9LF96	2 Q56337		11 Q9QYP2	4 092566		4 Q9HCU4	16 Q9KEL2	4 Q96CL0	3 Q96U x 9	5 Q9VWG4	16 Q9CHC5	5 Q9VWK3	3 013755
		Query	Length D	206	234	234	366	977	2144	2408	2920	2923	106	402	492	200	393	481	513
	dР	Query	Match	73.5	35.3	35.3	35.3	34.3	34.3	34.3	34.3	34.3	33.3	33.3	33.3	33,3	32.4	32.4	32.4
			Score	75	36	36	36	35	35	35	35	35	34	34	34	34	33	33	33
		Result	No.	-	7	е	4	Ŋ	9	7	æ	თ	10	11	12	13	14	15	16

			Q9tb48 platynereis	Q9hkz2 thermoplasm	09y506 homo sapien	O99vbl staphylococ		Q96x22 magnaporthe	Q8rmf0 streptococc		7	Q9bwq5 homo sapien	Q9fhi8 arabidopsis	neurc		шns	Q91zi0 mus musculu	Q9nyq7 homo sapien	088278 rattus norv	3		Q9u5a7 schistosoma	Q99jv7 mus musculu	Q20416 caenorhabdi	Q8xhe0 clostridium	Q9h6f9 homo sapien		P73992 synechocyst	067551 garlic late				•		10+0
																														ALIGNMENTS	•		206 AA.		Tant and and and atol
	926N60	P90821	Q9TB48	Q9HKZ2	09Y506	099VB1	09RCB5	Q96X22	O8RMF0	092201	Q9CF17	Q9BWQ5	Q9FHI8	однере	90XN60	035161	091210	Q9NYQ7	088278	Q9D2I3	P91256	Q9U5A7	Q99JV7	020416	овхнео	Q9H6F9	Q9D5Z1	P73992	067551	ALIGN			PRT;	Created)	Lagt con
	S	Ŋ	æ	17	4	16	2	c	7	æ	16	4	10	٣	4	11	1	4	11	11	Ŋ	Ŋ	11	2	16	4	11	16	12					15,	ď
	1086	312	308	347	355	373	406	419	439	492	512	774	877	1840	3014	3034	3301	3312	3313	148	528	260	.141						31				PRELIMINARY;	(TrEMBLrel.	(DI rol
•	32.4	31.9	31.4	31.4	31.4	31.4	31.4	31.4	31.4	31.4				31.4	31.4	31.4	31.4	31.4	31.4	30.9	30.9	30.9	30.4	30.4	30.4	30.4	30.4	30.4	\circ						
	33	2	~	7	2	2	. ~	32	7	7	~	7	7	2	7	7	7	7	7	'n.	2	r.	Н	1		7	31	31	31				IM3	01-OCT-2000	0000-500
	17	18	19	20	21	22	23	24	25	26	27	. 28	29	30	31	32	33	34	35	36	37.	38	39	40	41	42	43	44	45		RESULT 1	Σ	ID Q9NIM3		

PREJULY 1 OBONIM3 DE CONTINUARY; PRT; 206 AA. AC 090NIM3 DE COCT-2000 (TrEMBLrel. 15, Last sequence update) DT 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) DT 01-0CT-2000 (TrEMBLrel. 15, Last sequence update) DE Seroreactive antigen BMN1-17B. SEQUENCE TOWN (TREMBLrel. 15, Last annotation update) SEORGATION (TREMBLRel. 15, Last sequence update) NOBLINE-2000 (TREMBLRel. 15, Last sequence update) NOBLINE-2000 (TREMBLRel. 15, Last sequence update) RN NOBLINE-2001 (SEORGA N. 10, Reed S.G., Mohamath R., Reynolds I RA Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds I RA Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds I RA Benson D.R., Krause P.J., Reed S.G., Persing D.H.; RN MEDLINE-20031818; PubMed-10768973; RN MEDLINE-20031818; PubMed-10768973; RN MEDLINE-20031818; PubMed-10768973; RN MEDLINE-20031818; PubMed-10768973; SEQUENCE E.O. AA: 24963 MW; A287DESDBFD15C94 CRC64; SEQUENCE 206 AA: 24963 MW; A287DESDBFD15C94 CRC64; OUSPY MATCH SIMILARIY SIJS; Pred. NO. 7.5e-09; MATCHES INTERVSXSXXTFIXIXXXMXFFXXXXXFL 76 A5 RCLSITRFYSSISTFILIDFVMPFFTLFTYFL 76 RESULT 2 OUSPY WARD ACCOUNT (TERMBLREL 19, Created) DT 01-DEC-2001 (TERMBLREL 19, Created) DT 01-DEC-2001 (TERMBLREL 20, Last sequence update) DT 01-DEC-2001 (TERMBLREL 20, Last sequence update) DT 01-DEC-2001 (TERMBLREL 20, Last sequence update)

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Gaps

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7; Indels

Length 234;

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MEDLINE-96105201; PubMed-8529894;
Hardham J.W., Frye J.G., Stamm L.V.;
Hardham J.W., Frye J.G., Stamm L.V.;
Hidentification and sequences of the Treponema pallidum film', flir, flip, flio, fli and film genes.";
Gene 166:57-64(1995).
EMBL: U36899; AAB00549.1; -.
InterPro; IPR002066; Bac.export_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hardham J.M., Frye J.G., Young N.R., Stamm L.V.; "Sequences of the flhA, flhF, and orf304 genes of Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 2; Length 366;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases.
    to the EMBL/GenBank/DDBJ databases
                                                                                                     Interpro; IPR000866; AhpC-TSA.
Pfam; PF00578; AhpC-TSA; 1.
SEQUENCE 234 AA; 24684 MW; 4F66DA63CD15F003 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68DE94348679FF9A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01, Last sequence update)
21, Last annotation update)
                                                                                                                                                                                         35.3%; Score 36; DB 10; 43.8%; Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           776 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 CLSIXRFXXSXXTFIXIXXXMXFFXXXXXFL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Mismatches
                                                                                                                                                                                                                                2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
Submitted (JAN-2002) to the EM EMBL; AL132969; CAB86900.1; --
EMBL; AXV054638; AAK96829.1; --
EMBL; AXV05493; AAL66908.1; --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01312; Bac_export_2; PRINTS; PR00950; TYPE3IMSPROT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41733 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 311-366 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          35.3%;
25.8%;
                                                                                                                                                                                                                                                                         3 LSIXRFXXSXXTFIXI 18
                                                                                                                                                                                                                                                                                               5 LSVSRFMSSSATVISV 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01,
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01,
20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-312 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TIGREAMS; TIGRO0328; flhB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 25.0v
Local Similarity 25.0v
Local Similarity 25.0v
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
FlhB'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel. 01-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F14F11.1. Caenorhabditis elegans.
                                                                                                                                                                                                             Similarity 7; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      366 AA;
                                                                                      HSSP; P30044; 1HD2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F14F11.1 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-NICHOLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-NICHOLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                       Query Match
Best Local 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                         056337;
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                                                                                                                                                                                                                                                                                                                                                                                                                        056337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FLHB'
                                                                                                                                                                                                                                     Matches
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Q19464
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                                                                                                                                                               A Yamada K., Liu S.X., Pham P.K., Banh J., Banno F., Dale J.M.,

A Goldsmith A.D., Jiang P.K., Lee J.M., Onodera C.S., Quach H.L.,

A Tang C., Toriumi M., Yamamura Y., Yu G., Yu S., Bowser L., Jones T.,

A Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,

A Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E., Lam B.,

Lin J., Meyers M.C., Miranda M., Narusaka M., Nquyen M., Palim C.J.,

A Sakurai T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,

A Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;

"Full Length cDNA of gene FeJ2_130/AT3552960 (GI:7529720).";

Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.

B EMBL; AYG05880; AAR93817.1;

InterPro; IPR000866; AhpC-TSA.

R Pfam; PF00578; AhpC-TSA.

R Pfam; PF00578; AhpC-TSA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOUTBNICE FROM N.A.
SOUTBNICK A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Soutbwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
Chalm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
Sakurai T., Satou M., Saki M., Shinn P., Yamada K., Shinozaki K.,
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                       Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales, Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peroxiredoxin-like protein.
F8J2_130 OR AT3G52960, F8J2_130.
Arabidopsis thaliama (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Chenng M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Saki M., Shinn P., Yamada K., Shinozaki K., Ecker J., Theologis A., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,
Nyechselgartner M., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,
Quetier F., Salanoubat M.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 10; Length 234;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0cT-2000 (TrEMBLrel. 15, Created)
01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB 7
Pred. No. 4.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   234 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
    Putative peroxiredoxin protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LSIXRFXXSXXTFIXI 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                       NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9LF96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09LF96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 3
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation update)
75 CIGVLRFFFTRATTASIONTGWFFVFVRYFM 105
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Gaps

ö

19; Indels

us-09-853-079-36.rspt

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Nagase T., Seki N., Ishikawa K., Ohira M., Kawarabayasi Y., Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.; Frediction of the coding sequences of unidentified human genes. VI. the coding sequences of 80 new genes (KIAA0201 KIAA0280) deduced by analysis of CDNA clones from cell line KG-1 and brain."; I. SIMILARITY: CONTAINS 6 CADHERIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .
0
                                                                                                                                                                                                                                                                                                                                             PROSITE; PS00022; EGF_1; UNKNOWN_6.
PROSITE; PS01186; EGF_2; 4.
PROSITE; PS50227; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 11; Length 2144; 49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2144 AA; 233480 MW; 6EA898C1BA655ECA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-UTN-2002 (TrEMBLrel. 21, Last annotation update)
KIAA0279 protein (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3,
                                                                                                                                                              SMART; SM00112; CA; 3.
SMART; SM00179; EGE_CA; 1.
SMART; SM00001; EGE_Like; 6.
SMART; SM00001; GPS; 1.
SMART; SM00008; HORTME; 1.
SMART; SM00208; Lamne; 1.
PROSTER; PS00010; ASK_HYDROXYL; UNKNOWN_2.
PROSTER; PS00010; ASK_HYDROXYL; UNKNOWN_2.
PROSTEE; PS00010; ASK_HYDROXYL; UNKNOWN_2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 2408 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ouery Match 34.3%; Score 35; Best Local Similarity 54.5%; Pred. No. Matches 6; Conservative 2; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hormn_receptor.
Laminin_EGF.
Laminin_G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EGF_2.
EGF_Ca.
EGF_II.
GPCR_secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P15116; 1NCJ.
InterPro; IPR000152; Asx_hydroxyl.
InterPro; IPR002126; Cadherin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=97191544; PubMed=9039502;
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                                                                                                                                               GPCRSECRETIN.
                                                                           laminin_G; 1.
                                                                                                                              PRINTS; PR00011; EGFLAMININ.
   cadherin; 3.
                                                                                          PRINTS; PR00205; CADHERIN. PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                            ; PF02793; HRM; 1.
PF00054; lamin:-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         467 RCVSVLRFDSS 477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RCLSIXRFXXS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000561;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001791;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                 PR00249;
   PF00028;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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                                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    092566
     Pfam;
                                       Pfam;
Pfam;
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Q92566
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-SPRAGUE-DAWLEY: TISSUE-BRAIN;
Nakayama M., Nakajima D., Nagase T., Nomura N., Seki N., Ohara O.;
"Identification of high-molecular-weight proteins with multiple EGF-like motifs by moltf-trap screening.";
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: CONTAINS 4 CADHERIN DOMAINS.
-- EMBL, AB011529; BAA88687.1;
-- HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .;
0
                                                                                                                                                              Genome sequence of the nematode C.elegans: A.platform for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.3%; Score 35; DB 5; Length 776; illarity 33.3%; Pred. No. 21; Conservative 2; Mismatches 14; Indels
                                                    Lightning J , submitted (OCT-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87162 MW; 96A83E3FCBD25F93 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 2144 AA
                                                                                                                                                                                          Science 282:2012-2018(199).
Science 282:2012-2018(199).
EMBL; Z54307; CAA91092.1; -
InterPro; IPR001210; BTB_POZ.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR003969; K_channel.
InterPro; IPR003911; K_channel.
InterPro; IPR00311; K_channel.
InterPro; IPR00391; K_channel.
InterPro; IPR00391; K_channel.
InterPro; IPR003974; Shaw_channel.
Pfam; PF00169; Interpro; Pfam; PF00169; KCHANNEL.
PRINTS; PR01499; KCHANNEL.
PRINTS; PR01499; SHAWCHANNEL.
PRINTS; PR01499; SHAWCHANNEL.
SMART; SM00225; BTB; I.
SEQUENCE 776 AA; 87162 MW; 96A83E31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    255 CPSFHKFVRSPLTIIDVISTGAFF 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | IPR000742; EGF_2.
| IPR001481; EGF_Ca.
| IPR001488; EGF_III.
| IPR001832; GPCR_Secretin.
| IPR001879; hormn_receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 CLSIXRFXXSXXTFIXIXXXMXFF 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P00740; IEDM.
InterPro; IPR000152; Asx.hydroxyl.
InterPro; IPR002126; Cadherin.
InterPro; IPR000561; EGF-11ke.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR002049; Laminin_EGF.
IPR001791; Laminin_G.
IPR000203; PKD_cys_rich.
IPR001368; TNFR_C6.
                                                                                                                          MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21, MEGF3 (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001368; TNF
Pfam; PF00002; 7tm_2; 1.
                                                                                                                                                                                 investigating biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 8; Conserv
                                SEQUENCE FROM N.A.
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
NCBI_TaxID-6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9QYP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 6
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Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS0023; CADHERIN_1; 5.
PROSITE; PS0023; CADHERIN_1; 5.
PROSITE; PS0002; EGF_1; UNKNOWN_6.
PROSITE; PS01186; EGF_2; 2.
PROSITE; PS5027; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PS50261; G_PROTEIN_RECEP_F2_4; 1.
PROSITE; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
Calcium-binding; Cell adhesion; EGF_1ike domain; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34.3%; Score 35; DB 11; Length 2920;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2920 AA; 317648 MW; 2919558DF467114F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                O9HCU4;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                               SMARI, SM00303; GFS, L. SMART; SM00008; HOTMR; I. SMART; SM00008; HOTMR; I. SMART; SM00208; TMFR; I. SMART; SM00208; TMFR; I. PROSITE, PS00010; ASX_HYDROXIL; UNKNOWN_I. PROSITE; PS00212; CADHERIN_I; S. CADHERIN_2; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT; 2923 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | IPR000152; Asx_hydroxyl., |
| IPR001216; Cadherin., |
| IPR000761; EGF-1ike., |
| IPR000742; EGF-2., |
| IPR001881; EGF-2., |
| IPR001881; EGF-8ecretin., |
| IPR0018379; HORR.secretin., |
| IPR001879; HORR.secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001791; Laminin_G.
InterPro; IPR001203; PKD_cyg_rich.
InterPro; IPR001368; TNFR_c6.
Pfam; PF00002; 7tm_2; 1.
Pfam; PF00028; cadherin; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IPR002049; Laminin_EGF
                                                                                               Pfam; PF00008; EGF; 5.
Pfam; PF01025; GPS; 1.
Pfam; PF02193; HRM; 1.
Pfam; PF00054; laminin_G; 2.
PRINTS; PR00205; CADHERIN.
PRINTS; PR00011; EGFLAMININ.
                                                                                                                                                                                                                                                                   EGFLAMININ.
GPCRSECRETIN.
          IPR001368; TNFR_c6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                54.5%;
                                                                                                                                                                                                                                                                                                                                SWART; SW00112; CA; 9.
SWART; SW00180; EGE_Lam; 1.
SWART; SW00001; EGE_like; 6.
SWART; SM00303; GPS; 1.
                                     Pfam; PF00002; 7tm_2; 1.
Pfam; PF00028; cadherin; 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ||:|: || |
|1243 RCVSVLRFDSS 1253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 54.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RCLSIXRFXXS 11
                                                                                                                                                                                                                                                                                                         PRINTS; PR00249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLAMINGO 1.
             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9HCU4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
Q9HCU4
          NAME OF STREET O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 q
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MEDLINE=99418630; PubMed=10490098;

Usui T., Shima Y., Shimada Y., Hirano S., Burgess R.W., Schwarz T.L.,
Takeichi M., Uemura T.; transmembrane cadherin, regulates planar cell
polarity under the control of frizzled.";

Cell 98:585-595(1999).

-1- SIMILARITY: CONTAINS 9 CADHERIN DOMAINS.

BMBL, BAQ28499; BAA44070.1;

HSSP; P00740; IEDM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Flamingo 1.
CELSR2 OR FLAMINGO 1.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO0022; EGF_1: UNKNOWN_6.
PROSITE; PSO1186; EGF_2: 4.
PROSITE; PSO227; G_PROTEIN_RECEP_F2_3; 1.
PROSITE; PSO2026; G_PROTEIN_RECEP_F2_4; 1.
PROSITE; PSO1248; LAMININ_IYPE_EGF; UNKNOWN_1.
Calcium-binding; Cell adhesion; EGF-like domain; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35; DB 4; Length 2408; Pred. No. 54; Aismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2408 AA; 261739 MW; EF4BFC2CF993355F CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              SMART; SM00179; EGE_CA; 1.
SMART; SM00101; EGE_Like; 6.
SMART; SM00303; GPS; 1.
SMART; SM00282; LamG; 2.
SMART; SM00282; LamG; 2.
SMART; SM00282; LamG; 2.
PROSITE; PS00010; ASX_HYDROXYL; UNKNOWN_2.
PROSITE; PS00232; CADHERIN_1; 3.
PROSITE; PS0058; CADHERIN_1; 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT; 2920 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
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InterPro; IPR00199; Laminin_EGF.
InterPro; IPR001791; Laminin_G.
InterPro; IPR000203; PKD_cys_rich.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGF_2.
GPCR_secretin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000152; Asz_hydroxyl.
InterPro; IPR002126; Cadherin.
InterPro; IPR000561; EGF-like.
InterPro; IPR000203; PKD_cys_rich.
InterPro; IPR001368; TNFR_c6.
                                                                                                                          Pfam; PF00008; EGF; 6.
Pfam; PF01825; GPS; 1.
Pfam; PF0273; HRM; 1.
Pfam; PF00054; laminin_G; 1.
PRINTS; PR00205; CADHERIN.
PRINTS; PR00010; EGFBLOOD.
                                                                                                                                                                                                                                                                                                                                PRINTS, PRODO11; EGFLAMININ.
SWART; SM00112; CA; 6.
SWART; SM00179; EGF_CA; 1.
SWART; SM0001; EGF_11ke; 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34.3%;
ilarity 54.5%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                      cadherin; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MGD; MGI:1858235; Celsr2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 RCVSVLRFDSS 737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RCLSIXRFXXS 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9R0M0
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Q9R0M0
      g
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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hebeloma cylindrosporum.
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Cortinariaceae; Hebeloma.
NCBI_TaxID=76867;
                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
L Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; BOOH161; AMH14161.;
R INTELPTO: IPR001099; KRAB.
R InterPro; IPR001099; Znf_C2H2.
R PRositE; PS50805; Znf_C2H2.
R PROSITE; PS50805; XRAB; 11.
R PROSITE; PS50157; ZINC_FINGER_C2H2_1; UNKNOWN_11.
R PROSITE; PS50157; ZINC_FINGER_C2H2_2; 11.
RW DNA-binding; Hypothetical protein; Zinc-finger.
SQ SEQUENCE 402 AA; 45857 MW; 824FBABAF66609C1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   33.3%; Score 34; DB 4; Length 402; 37.5%; Pred. No. 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS01219; AMMONIUM_TRANSP; UNKNOWN_1.
SEQUENCE 492 AA; 53673 MW; 83E8B1227DFE4064 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
Last sequence update)
Last annotation update)
                                                                                                                                                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-UNI-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 45.9 kba protein.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
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Pred. No. 23;
4; Mismatches 13
                                                                                                        402 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                492 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LSIXRFXXSXXTFIXIXXXMXFF 25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11: :| ||||
148 RCIECGKFLKKHSTFI 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.3%;
30.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RCLSIXRFXXSXXTFI 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-DEC-2001 (TrEMBLrel. 19, 01-DEC-2001 (TrEMBLrel. 19, 01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 37.5
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-SKIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                  0396C
                                                                                                                                   096CL0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6XN960
                                                 RESULT 11
Q96CL0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 12
Q96UX9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dp
                                                                                                                                   DDT TENER BY THE POST OF THE P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N. Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
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NCBL_TaxID=86665;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34; DB 16; Length 106;
Pred. No. 6.3;
1; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 4; Length 2923;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Calcium-binding; Cell adhesion; Glycoprotein.
SEQUENCE 2923 AA; 317447 MW; 382757D315158ED8 CRC64;
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SEQUENCE 106 AA; 11537 MW; 23BE07040ECBF303 CRC64;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                       SM00008; HOTMR; 1.
SM00208; THRP; 1.
SM00208; THRPR; 1.
S. PS00010; ASX HYDROXXL; UNKNOWN_1.
E; PS00232; CADHERIN_1; 6.
E; PS00222; EGF_1; UNKNOWN_6.
E; PS01186; EGF_2; 4.
E; PS01248; G_PROTEIN_RECEP_F2_3; 1.
E; PS50261; G_PROTEIN_RECEP_F2_4; 1.
E; PS01248; LAMININ_TYPE_EGF; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00893; DUF7; 1.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   106 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35; DB 4
Pred. No. 64;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; Pubmed=11058132;
                                                                                               PRINTS; PR00205; CADHERIN.
PRINTS; PR00011; EGFLAMININ.
PRINTS; PR00249; GPCRSECRETIN.
SMART; SM00112; CA; 9.
SMART; SM001011; EGF; 8.
SMART; SM00101; EGF; 8.
SMART; SM00101; EGF; 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AP001510; BAB04559.1; ...
InterPro; IPR000390; DUF7.
InterPro; IPR001092; HLH_basic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Multidrug resistance protein.
                   Pfam; PF01825; GPS; 1.
Pfam; PF02793; HRM; 1.
Pfam; PF00054; laminin_G; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
34.3%;
Best Local Similarity 54.5%;
Matches 6; Conservative
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|1242 RCVSVLRFDSS 1252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 RCLSIXRFXXS 11
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Best Local Similarity
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                                                                                                                                                                                                                                                                                    SM00303;
SM00008;
SM00282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PSO0022
PROSITE; PS01186
PROSITE; PS50227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROSITE; PS50261
Pfam; PF00008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Horikoshi K.;
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PROSITE;
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SMART;
SMART;
SMART;
SMART;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9KEL2
                                                                                                                                                                                                                                                                                                                                                                    SMART;
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SO ON THE PROPERTY OF THE PROP
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Query Match
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                                   Q9CHC5
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Q9VWK3
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RESULT 14
                  Q9CHC5
                                     Dp
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RA Adams M.D., Celniker S.E., 11 P.W., Hoskins R.A., Galle R.F.,
Gocaye R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortnan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Baradon R.C., Rogars Y.H.C., Blazej R.G., Champe M., Pfelffer B.D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Benca P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brystataroglu L., Beasley E.M.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gody E.E., Downes M., Dugan-Rocha S., Pleischman W.,
RA Glodek A., Gody E., Gorrell J.H., Gu Z., Gelbart W.M., Classer K.,
RA Glodek A., Gody F., Gorrell J.H., Gu Z., Gelbart W.M., Classer R.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodire C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
Lasko P., Leil Y., Levitsky A.A., Li Z., Liang Y., Lin X.,
RA Mount S.M., Moy W., Murphy B., Murphy L., Murzhy D.M., Nelsen D.L.,
Ralus R., Reinert K., Remindton K.J., Power D., Worled M.P., Morles D.M.,
Ralus R., Reiner R., Sanden Kiamos I., Simpson M., Skupski M.P., Sanith T.,
Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Sanith T.,
Ra Spier E., Spradling A.C., Stapleton M., Zhong G., Zhao Q., A.,
Walliams S.M., Woodage T., Worley C., Wu D., Yang S., Zhao Q., A.,
Ra Heinert K., Benington R., Zhao M., Zhong G., Zhao Q., Zhao K., Heins S., Lhue S., Cheeler F., Shen E.,
Ra Heinert K., Benington M., Zhong G., Zhao Q., Zhao R., Karissenberd J.,
Ra Heinert K., Remington R., Zhao M., Zhang S., Zhao W., Zhao Q., Zhao S., Zhao M., Zhang S., Zhao S., Zhao M., Zhang S., Zhao S., Zhao S., Zhao S., Zhao S., Zhao S., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Tracheata, Hexapoda, Insecta,
Pterygota; Neoptera, Endopterygota; Diptera; Brachycera, Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Interpro; IPR002656; Acyl_transf_3.
Pfam; PF01757; Acyl_transf_3; 1.
SEQUENCE 700 AA; 78477 MW; 3514BF1A51A43610 CRC64;
                                                                                                   01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                            MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FlyBase; FBqn0031034; CG14205
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                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                        CG14205 protein.
                                                                                                                                                                                                                                                                       NCBI_TaxID=7227;
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                                                                                      Q9VWG4;
                                                                   Q9VWG4
                                 RESULT 13
                                                    Q9VWG4
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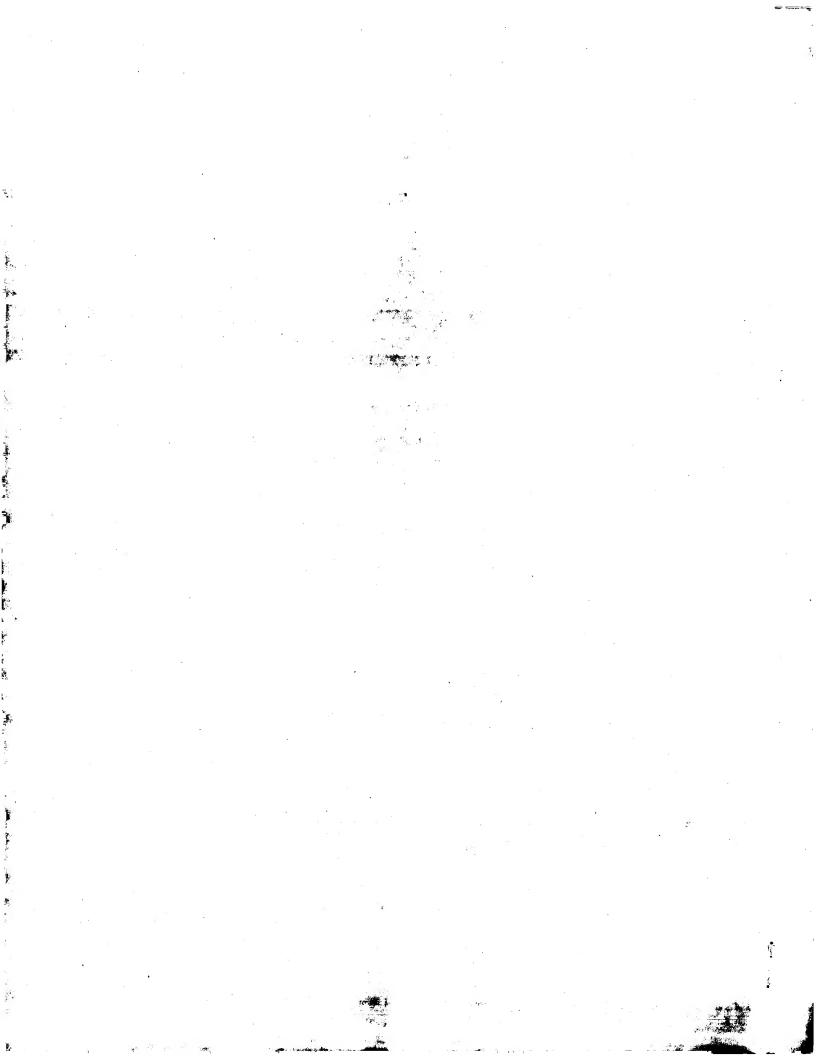
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Annaritdes P.G., Scherer S.E., Li P.W., Hoskins K.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA ADril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Berman B.P., Bhandrai D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davis S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burbin K.J., Evangelista C.C., Ferraz C., Ferriara S., Fleischmann W.,
R. Fosler C., Gabriellan A.E., Garg N.S., Gelbart W.M., Glasser K.,
Allodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
Ray Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                              STRAIN-IL1403,
MEDLINE-21235186; PubMed=11337471;
MEDLINE-21235186; PubMed=11337471;
MEDLINE-21235186; PubMed=11337471;
Meissenbach J., Bhrlich S.D., Sorokin A.;
"The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp. lactis IL1403.";
Genome Res. 11:731-75(2001).
EMBL; AE006314; AAK04905.1;
InterPro; IPR001117; Cu-oxidase.
PROSITE; PS00079; MULTICOPPER_OXIDASE1; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                  Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            393 AA; 43617 MW; 3BD755460656204C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-WAY-2000 (TrEMBLrel. 13, Created)
01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5; Mismatches
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| 154 ISFERFRASIFLFLSLVLNLLYF 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 LSIXRFXXSXXTFIXIXXXMXFF 25
                                                                                                                                                                                                                          Streptococcaceae; Lactococcus.
                                                                    01-JUN-2001 (TrEMBLrel. 17, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6; Conservative
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome. SEQUENCE 393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                       Unknown protein.
YIBE OR LL0807.
                                                                                                                                                                                                                                              NCBI_TaxID=1360;
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                                             01-JUN-2001
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RA Hostin D., Houston K.A., Howland T.J.; Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kadraa C.D., Kraft C., Kravitz S., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lel Y., Levitsky A.A., Li J., Li Lang Y., Lin Z.,
RA Lux X., Mattei B. McIntcsh T.C., McLeod M.P., McPherson D.,
RA McIshib B., McIntcsh T.C., McLeod M.P., McShrefi A.,
RA McIson D.R., Malson K.A., Nixon Y. D.M., Nelson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nalson K.A., Nixon X., Nisskern D.R., Pacled J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri Y. Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spice E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spice E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Syirskas R., Tector C., Turner R., Venter E., Mang A.H., Wang X.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA G.J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA C.J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA G.J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao C., Zheng L.,
RA G.J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao C., Zheng E.,
R. Science 287:2185-2195(2000)
R. RHBL, AEC03511; AAR48935:1;
R. Science 287:2185-2195(2000)
R. RHBL, REOUSST; Chitin_bind_Pera.
R. Shark; SMO494; ChEBZ; J.
SQUERCE 481 AA, 50912 WW; 4E3F0A7C6241AC4E CRC64;
Ratches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
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Search completed: July 16, 2003, 17:49:59 Job time : 10.7707 secs

2 CLSIXREXXSXXTF 15 |||:|| || 342 CLSVGRFAGIDETY 355

상 음



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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 16, 2003, 17:36:24 ; Search time 8.95784 Seconds Run on:

(without alignments)
476.010 Million cell updates/sec

US-09-853-079-39 108 1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

908470 segs, 133250620 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :

1. SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT:*
2. [SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:*
3. [SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:*
3. [SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:*
3. [SIDS2/gcgdata/geneseqy-embl/AA1981.DAT:*
3. [SIDS2/gcgdata/geneseqy-embl/AA1984.DAT:*
3. [SIDS2/gcgdata/geneseqy-embl/AA1986.DAT:*
3. [SIDS2/gcgdata/geneseqy-embl/AA1986.DAT:*
3. [SIDS2/gcgdata/geneseqy-embl/AA1980.DAT:*
3. [SIDS2/gcgdata/geneseqy-embl/AA1980.DAT:*
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5. [SIDS2/gcgdata/geneseqy-embl/AA1980.DAT:*
6. [SIDS2/gcgdata/geneseqy-embl/AA1990.DAT:*
6. [SIDS2/gcgdata/geneseqy-embl/AA1990.DAT:* A_Geneseq_101002:*

18: 19:

/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1999.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA2000.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* /gcgdata/geneseq/geneseqp-emb1/AA2001

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMALES	
		æ				
Result		Query				
No.	Score	Match	e Match Length DB ID	DB	ID	Description
		1 1 1 1		:		
П	82	75.9	445	19	AAW56298	Babesia microti BM
7	82	75.9		20	AAY24358	Babesia microti an
e	82	75.9		21	AAB30207	B. microti BMNI-17
4	82	75.9		23	ABB88952	Babesia microti an
S	82	75.9		23	ABB89025	Babesia microti an
9	82	75.9		21	AAB30230	B. microti MN-10/B
7	82	75.9		23	~	Babesia microti an
80	82	75.9	677	23	~	Babesia microti an
6	82	75.9	М	21	AAB30231	B. microti MN-10/B
10	82	75.9	_	23	ABB88976	Babesia microti an

Babesia microti an Babesia microsyl S. mutans glucosyl S. mutans glucosyl Drosophila melanog Babesia microti an S. epidermidis ope Staphylococcus epi	and microci enitalium y l human dia l kinase (P ophila mela ne PCLP1. l protein s a-ketogluta
AAY 24359 AAB30208 ABB8953 AAW56303 AAY 24365 AAB30217 ABB89012 ABB89012 ABB89012 ABB89010 ABB89011 ABC05779 AAU98043 AAU98043 AAU98044 AAU98045	AANY 55637 AAY 55637 ABC 03617 AAE 6410 AAB 980 AAB 980 AAY 31988
335355555555555555555555555555555555555	505555555555555555555555555555555555555
32 32 32 32 32 32 32 32 32 32 32 32 32 3	23 367 398 735 400 503 914 407
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88 80 90 90 90 90 90 90 90 90 90 90 90 90 90	
112 112 112 113 114 115 116 117 117 117 117 117 117 117 117 117	23337 7444444444444444444444444444444444

ALIGNMENTS

antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrllchiosis. Babesia microti BMNI-17 complement antigen sequence. AAW56298 standard; Protein; 445 AA 97EP-0117067. 97US-0845258. 96US-0723142. 28-SEP-1998 (first entry) (CORI-) CORIXA CORP Babesia microti. 01-OCT-1997; 24-APR-1997; 01-OCT-1996; EP834567-A2. 08-APR-1998. AAW56298; RESULT 1 AAW56298

Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, WPI; 1998-195465/18. N-PSDB; AAV22753

Sleath PR;

Reed SG,

Houghton R, Lodes MJ,

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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                in a patient
              Query Match
Best Local Similarity
Thes 18; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lodes MJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                     (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                             Babesiosis; rodent
                                                                                                                                                                                                                                                                          disease diagnosis;
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nes 18; Conser
  445 AA;
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                                                                                                                                                                                                                                                                                                                                                12-OCT-2000.
                                                                                                                                                                                      AAB30207;
   Sequence
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                                                                                                                                       RESULT 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Babesia microti antigen BMNI-17 complementary open reading frame protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88983 to AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAV24327 to AAV2438 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence encodes a B.microti antigen.
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
transformed cells and antibodies, useful for diagnosis of
                                                      The sequence is that of a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:
(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichlosis) that have similar symptoms but require different treatments.
                                                                                                                                                                                                                                                                         ;
                                                                                                                                                                                                                                               Length 445;
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                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                               Score 82; DB 19;
Pred. No. 5.5e-09;
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                                                                                                                                                                                                                                                                                               . 1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                        0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated Babesia microti polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 91-92; 126pp; English.
              infection and in protective vaccines
                                  Claim 1; Page 77-79; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                 AAY24358 standard; Protein; 445 AA.
                                                                                                                                                                                                                                              75.98;
56.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97US-0990571,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-US26437
                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                           Best_Local Similarity 56.2
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MAYO-) MAYO FOUNDATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-385612/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunity; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CORI-) CORIXA CORP
                                                                                                                                                                                                                       445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAX90012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Babesia microti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09929869-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUN-1999
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                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                      B. microti BMNI-17 antigen reverse complement SEQ ID NO: 38.
Length 445;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                  parasite; tick-borne illness; antigen; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McNeil1
Score 82; DB 20;
Pred. No. 5.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5.5e-09;
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                                                                                                                244 GHDKINKNKSGNAGIKSYDTQTPQETSDAHEE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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Pred. No. 5.5e-
0; Mismatches
                                            Mismatches
                                                                                       1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE
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                                                                                                                                                                                                                                                AAB30207 standard; Protein; 445
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75.9%;
56.2%;
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56.2%;
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17-MAR-2000; 2000US-0528784.
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Homer MJ;

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The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                           New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections \,
                                                                                                                      McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McNeill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Babesiosis; rodent parasite; tick-borne illness; antigen; disease diagnosis; disease prevention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        B. microti MN-10/BMNI-17 fusion protein SEQ ID NO: 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 23;
6e-09;
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                                                                                                                      Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          280 GHDKINKNKSGNAGIKSYDTQTPQETSDAHEE 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 82; DB 2
Pred. No. 6e-09
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 7; Page 108-111; 118pp; English
                                                                                                                                                                                                                                                                                  Claim 2; Page 191-192; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA.
                                                                                                                      Lodes MJ, Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB30230 standard; Protein; 666
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56.2%;
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17-MAR-2000; 2000US-0528784
              10-OCT-2000; 2000US-0685436.
13-DEC-2000; 2000US-0737178.
26-FEB-2001; 2001US-0794764.
07-SEP-2000; 2000US-0656688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 56.29
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                                                                                       (CORI-) CORIXA CORP
                                                                                                                                                                          WPI; 2002-216691/27
                                                                                                                                                                                                                                                                                                                                                                                                                                               481 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Babesia sp.
Synthetic.
                                                                                                                                         Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB30230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reed SG,
                                                                                                                          SG,
                                                                                                                          Reed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 6
AAB30230
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                             Homer MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  infection. The present sequence was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Babesia microti antigens, useful for diagnosing and treating B microti infection, and as component of a composition for enhancing immune response against B. microti infections
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                                                     Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                                                                                                                                                                                                            McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.9%; Score 82; DB 23; Length 445; 56.2%; Pred. No. 5.5e-09; Live 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Babesia microti antigenic epitope fusion protein.
                                                                                                                                                                                                                                                                                                                                                                                            Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               244 GHDKINKNKSGNAGIKSYDTQTPQETSDAHEE 275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; Page 92-93; 195pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABB89025 standard; Protein; 481 AA
                  Babesia microti antigen epitope #1.
                                                                                                                                                                                                                                                                                                                                                                                            Lodes MJ, Houghton RL,
                                                                                                                                                                                                                                               2000US-0605724.
2000US-0656688.
2000US-0685436.
2000US-0737178.
2001US-0794764.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 75.9
Best Local Similarity 56.2
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-216691/27.
                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Babesia microti.
                                                                                       Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200185947-A2.
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07-SEP-2000;
10-OCT-2000;
13-DEC-2000;
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                                                                                                                                                           15-NOV-2001
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Secrist H;
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ABB8902 RESULT

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New Babesia microti antigens, useful for diagnosing and treating B microti infection, and as component of a composition for enhancing
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                                                                                                                                                                                           Babesia microti antigenic epitope fusion protein BaF-5.
microti infection, and as component of a compound immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lodes MJ, Houghton RL,
                                                                                            ABB88989 standard; Protein; 677
                                                                                                                                                                                                                                                                                                                                                                                                     27-JUN-2000; 2000US-0605724.
07-SEP-2000; 2000US-0556688.
10-OCT-2000; 2000US-0685436.
13-DEC-2000; 2000US-0737178.
26-FEB-2001; 2001US-0794764.
                                                                                                                                                                                                                                                                                                                                                       09-MAY-2001; 2001WO-US15192
                                                                                                                                                                                                                                                                                                                                                                                       2000US-0569098
                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           677 AA;
                                                                                                                                                                                                                                                                                        WO200185947-A2.
                                                                                                                                                                                                                                                                                                                                                                                       10-MAY-2000;
                                                                                                                                                            20-JUN-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Reed SG, Secrist H;
             465
                                                                                                                          ABB88989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                             ABB88989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
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          The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homer MJ;
                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Babesia microti antiqens, useful for diagnosing and treating B microti infection, and as component of a composition for enhancing immune response against B. microti infections
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                            Length 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 666;
                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                   Babesia microti antigenic epitope fusion protein BaF-3.
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. 8.8e-09;
. 14;
                                                                                                                                                        Score 82; DB 21; L
Pred. No. 8.8e-09;
0; Mismatches 14;
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                                                                                                                                                                                                                                            1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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Pred. No. 8.8e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 35; Page 113-115; 195pp; English.
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                                                                                                                                                                                                                                                                                                                                     ABB88975 standard; Protein; 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000US-0569098.
2000US-0605724.
2000US-065688.
2000US-0685436.
2000US-0731778.
                                                                                                                                                        75.9%;
56.2%;
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56.2%;
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                                                                                                                                                        Query Match 75.9 Best Local Similarity 56.2 Matches 18; Conservative
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nes 18; Conservative
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                                                                                                                          666 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     666 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200185947-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protozoacide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUN-2000;
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13-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Secrist H;
                                                                                                                                                                                                                                                                                                                                                                     ABB88975;
                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                     RESULT 7
                                                                                                                                                                                                                                                                                                                      ABB88975
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Homer MJ;

McNeill PD,

Sleath PR,

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                                        The present invention relates to novel Babesia microti antigens and to coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              87.
                                                                                                                                                                                                                                                   Length 677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B. microti MN-10/BMNI-17/BMNI-15 fusion protein SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babesiosis; rodent parasite; tick-borne illness; antigen;
                                                                                                                                                                                                                                                                        8.9e-09;
                                                                                                                                                                                                                                                   Score 82; DB 23;
Pred. No. 8.9e-09;
0; Mismatches 14
                                                                                                                                                                                                                                                                                                                                                                          GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
Claim 35; Page 160-163; 195pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB30231 standard; Protein; 1132 AA
                                                                                                                                                                                                                                                   75.98;
56.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                        Best Local Similarity 56.2
Matches 18; Conservative
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1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32

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The present invention relates to novel Babesia microti antigens and to coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                     Homer MJ;
                                                                                                           New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
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                                                                                                                                                                                                                                                                                                                                                                                                    Length 1132;
                   McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Babesia microti antigen BMNI-17 degenerate repeat sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                  75.9%; Score 82; DB 23; 56.2%; Pred. No. 1.6e-08;
                   Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Mismatches
                                                                                                                                                                                        Page 116-120; 195pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
3
                     Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
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Misc-difference 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'label= Gly, Asp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= Lys, Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         label= Glu, Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             label= Ile, Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       label= Thr, Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           label= Ilr, Thr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY24359 standard; peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'label= Lys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= Asp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      label= Pro,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                Query Match 75.9
Best Local Similarity 56.2
Matches 18; Conservative
                       Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunity; detection.
                                                                        WPI; 2002-216691/27
                                                                                                                                                                                                                                                                                                                                                               1132 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16-SEP-1999
                                       Secrist H;
                                                                                                                                                                                          Claim 35;
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY24359;
                     Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                           New polypeptides containing an antigenic portion of Babesia microti
antigen and DNAs encoding the polypeptides, useful for diagnosing,
treating or preventing B. microti infection, or for inducing protective
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1132;
                                                                                                                                                                                                                                                                                                        McNeill PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Babesia microti antigenic epitope fusion protein BaF-3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 82; DB 21;
Pred. No. 1.6e-08;
                                                                                                                                                                                                                                                                                                    Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 7; Page 112-116; 118pp; English.
disease diagnosis; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABB88976 standard; Protein; 1132 AA
                                                                                                                                                                                                                                                                                                    Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     75.9%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0605724.
2000US-0656688.
2000US-0685436.
2000US-0737178.
2001US-0794764.
                                                                                                                                                                  05-APR-2000; 2000WO-US09136
                                                                                                                                                                                                      05-APR-1999; 99US-0286488
17-MAR-2000; 2000US-0528784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-MAY-2001; 2001WO-US15192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 56.2
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       in a patient
                                                                                                                                                                                                                                                                                                                                       WPI; 2000-686939/67.
                                                                                                                                                                                                                                                               (CORI-) CORIXA CORP.
                                                                                                                                                                                                                                                                                                    Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Babesia microti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200185947-A2.
                                                                                        WO200060090-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27-JUN-2000;
07-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-NOV-2001
                                                                                                                             12-OCT-2000
                                   Babesia sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                       .mmunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB88976;
                                                                                                                                                                                                                                                                                                    Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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09-MAY-2001; 2001WO-US15192.
                                                                                                                                               Local Similarity
les 32; Conser
                                                                                                                     32 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
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                                                                                                                                                                                                                                                                                                                                  Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200185947-A2
                                                                                                                                                                                                                                                                             20-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-NOV-2001
                                                                                                                       Sequence
                                                                                                                                                                                                                                                           ABB88953;
                                                                                                                                      Query Match
                                                                                                                                                        Matches
                                                                                                                                                                                                                       RESULT 13
                                                                                                                                                                                                                                 ABB8895
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                                                                                                                                                                                                 The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88983 to AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAX4327 to AAX24338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. They microti infections. The present sequence represents a B.microti antigen BMNI-17 degenerate repeat sequence.
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polypeptides containing an antigenic portion of Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                             B. microti BMNI-17 antigen reverse complement repeat SEQ ID NO: 39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PD;
                                                                                                                                                                                                                                                                                                       Length 32;
                                                                                                                     SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                parasite, tick-borne illness; antigen; disease prevention.
                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                     Reed
                                                                                                                                                                                                                                                                                                      DB 20; I
7.1e-10;
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                                                                                                                     Persing
                                                                                                                                                                                                                                                                                                                                                    1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                      Score 80; DB;
Pred. No. 7.16
0; Mismatches
                                                                                                                                                                New isolated Babesia microti polypeptides
                                                                                                                     Lodes MJ,
                                                                                                                                                                                  Example 1; Page 94; 126pp; English
                                                                                                                                                                                                                                                                                             74.1%; Scor.
100.0%; Pred
0; }
                                                                                                                                                                                                                                                                                                                                                                                                        AAB30208 standard; Peptide; 32 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghton RL,
/label= Cys, His
                                                      98WO-US26437
                                                                       97US-0990571
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17-MAR-2000; 2000US-0528784
                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                     Houghton R,
                                                                                                                                                                                                                                                                                                                        32; Conservative
                                                                                                   (MAYO-) MAYO FOUNDATION
                                                                                                                                               WPI; 1999-385612/32.
                                                                                          (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-686939/67
                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babesiosis; rodent
disease diagnosis;
                                                                                                                                                                                                                                                                                    32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200060090-A1.
                  W09929869-A1
                                                      11-DEC-1998;
                                                                       11-DEC-1997;
                                                                                                                     Bruinsma E,
                                                                                                                                                                                                                                                                                                                                                                                                                                           12-FEB-2001
                                    17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2000
                                                                                                                              Sleath PR;
                                                                                                                                                                                                                                                                                     Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                          AAB30208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SG,
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antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient \,
                                                                                                                               The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted thumans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protozoacide; vaccine; antigen; antigenic epitope; infection
                                                                                                                                                                                                                                                                                                                                          Length 32;
                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                       ore 80; DB 21;
red. No. 7.1e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babesia microti antigen epitope repeat.
                                                                                                                                                                                                                                                                                                                                          Score 80;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ą.
                                                                                        Claim 6; Page 88; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _{
m Thr}
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                                                                                                                                                                                                                                                                                                                                       74.1%; SC ilarity 100.0%; P Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABB88953 standard; Peptide; 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= Gly,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label= Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Lys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  label= Glu,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        label= His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    label= Thr,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              label= Ile,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cys,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label= Glu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /label= Cys,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                label=
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Gaps

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14; Indels

32

Score 79; DB 19; Pred. No. 1.4e-08; 0; Mismatches 14.

Length 275;

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one addition to portion of a Babbsia microti antigen. Trean be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection by detecting specific antibodies in usual immunoassays. Infection by detecting specific antibodies of probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
                                                 sequence is that of a polypeptide comprising at least
                                                                                                                                                                                                                                                                                       1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE
                         Claim 1; Page 101-102; 113pp; English.
infection and in protective vaccines
                                                                                                                                                                                                                                      73.18;
56.28;
                                                                                                                                                                                                                                                 Best_Local Similarity 56.2
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-385612/32.
N-PSDB; AAX90017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunity; detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORI-) CORIXA CORP
                                                                                                                                                                                                             275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9929869-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-JUN-1999.
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                                                                                                                                                                                                                                                                                                                                                                                                   AAY24365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                    RESULT 15
                                                                                                                                                                                                                                                                                                                                                               AAY 24365
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                                                                                                                                                                                                                                                            The present invention relates to novel Babesia microti antigens and their
                                                                                                                                                                                                                                                                       coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                          Homer MJ;
                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                  New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.
                                                                                                                        McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                           Length 32;
                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                             Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                           1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Babesia microti BMNI-20 antigen sequence.
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                                                                                                                        Houghton RL,
                                                                                                                                                                                                                                                                                                                                                               74.1%; Scor.
100.0%; Pre
0;
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                                                                                                                                                                                                                                    Claim 7; Page 94; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW56303 standard; Protein; 275
          10-MAY-2000; 2000US-0569098.
27-JUN-2000; 2000US-065524.
07-SEP-2000; 2000US-0656688.
10-OCT-2000; 2000US-0685436.
13-DEC-2000; 2000US-0731778.
26-FEB-2001; 2001US-0794764.
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96US-0723142.
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                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
ماکنه 32; Conserva
                                                                                                                        Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-195465/18.
                                                                                               (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORI-) CORIXA CORP
                                                                                                                                                            WPI; 2002-216691/27
                                                                                                                                                                                                                                                                                                                                                 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAV22749
                                  07-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24-APR-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-APR-1998
                                                                                                                                      Secrist H;
                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW56303;
                                                                                                                        Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 14
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Babesia microti antigen BMNI-20 complementary open reading frame protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes isolated polypeptides comprising
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New isolated Babesia microti polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Page 109-110; 126pp; English.
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0; Gaps Query Match
73.1%; Score 79; DB 20; Length 275;
Best Local Similarity 56.2%; Pred. No. 1.4e-08;
Matches 18; Conservative 0; Mismatches 14; Indels

. 0

1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32

216 GHGKPNTNKSEKAERKSHDTQTTQEICEECEE 247

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Search completed: July 16, 2003, 17:46:44 Job time: 9.95784 secs

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July 16, 2003, 17:42:54; Search time 2.914 Seconds (without alignments) 323.107 Million cell updates/sec
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/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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108
1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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                                                                                                                                                                                                                                                                                                                                                                     262574 seqs, 29422922 residues
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Maximum Match 1008
Listing first 45 summaries
                                                                                    OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                Title:
Perfect score:
Sequence:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 38, Appl Sequence 38, Appl Sequence 38, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 54, Appl Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 10, Appli Sequence 10, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli	•
SUMMARIES	US-08-845-258-38 US-08-900-571-38 US-09-528-7448-38 US-09-528-7448-87 US-09-528-7448-87 US-08-990-571-39 US-08-990-571-39 US-08-990-571-39 US-08-990-571-53 US-08-990-571-53 US-08-990-571-53 US-09-900-571-53 US-09-900-571-53 US-09-174-6 US-09-174-6 US-09-174-6 US-09-174-10 US-09-174-388-10 US-09-271-4388-10 US-09-271-4388-10 US-09-134-001C-5080 US-09-134-001C-5080 US-09-134-001C-5080 US-09-134-001C-5080 US-09-134-001C-5080 US-09-134-001C-5080 US-09-134-001C-5080 US-09-134-001C-5080 US-09-134-001C-5080 US-09-134-001C-5080 US-09-134-01C-5080 US-09-134-01C-5080 US-09-134-01C-5080 US-09-134-01C-5080 US-09-134-01C-5080 US-09-134-01C-5080 US-09-134-01C-5080 US-09-134-01C-5080 US-09-134-01C-5080 US-09-134-01C-5080 US-08-482-271-3	
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264 264 264 264 264 272 291 291 291 293 311 112 112 115 115	ALIGN ilication US/08845258 feed, Steven G. odes, Michael J. oughton, Raymond leath, Paul R. NTION: COMPOUNDS AND NTION: DOUGHOUS S. EADDRESS: SEED AND BERRY 00 Columbia Center, 70; tile hington SA ABLE FORM: FLOPPY disk FLOPPY disk FLOPPY disk FLOPPY disk FLOPPY disk COMPALIANE COMPALIANE SA ABLE FORM: SA	75.9%; Score 82; D imilarity 56.2%; Pred. No. 1 Conservative 0; Mismatche. GHXKXNXNKSXXAXXKSXDTQTXQEXXXXEE
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	T 1 -845-258-38 uence 38, Application US/0884; ent No. 6183976 APPLICANT: Reed, Steven G. APPLICANT: Lodes, Michael J. APPLICANT: Lodes, Michael J. APPLICANT: Sleath, Paul R. TITLE OF INVENTION: COMPOUNDS TITLE OF INVENTION: AND TREA NUMBER OF SEQUENCES: 53 CORRESPONDENCE ADDRESS: ADDRESSEE: SEED AND BERRY STREET: 6300 Columbia Cent. CITY: Seattle CITY: Seattle CITY: Washington COUNTRY: USA ZIP: 9810 N AND ADARS MEDIUM TYPE: Floppy disk COMPUTER: TBM PC COMPALIBLE OPERATING SYSTEM: PC-DOS/WN SOFTWARE: PATENTIN RELEASE CURRENT APPLICATION NUMBER: US/08/FILING DATE: 24-APR-1997 CLASSIFICATION NUMBER: 31,39; REGISTRATION NUMBER: 31,39; REGISTRATION NUMBER: 24-000 TELEPHONE: (206)62-6031 TELEFONMUNICATION INFORMATION TELEFONMUNICATION INFORMATION TELEFONGE: (206)62-6031 TELEFONGE: (206)62-6031 TELEFONGE: (206)62-6031 TYPE: amino acids STYPE: amino acids STYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: 386	/ Match Local nes 1
2222 2222 2333333333333333333333333333	SULT 1 -08-845-258-38 Sequence 38, Application US/088452 Patent No. 6183976 GENERAL INFORMATION: APPLICANT: Reed, Steven G. APPLICANT: Reed, Steven G. APPLICANT: Boughton, Raymond APPLICANT: Gleath, Paul R. TITLE OF INVENTION: COMPOUNDS TITLE OF INVENTION: AND TREATH NUMBER OF SEQUENCES: 53 CORRESPONDENCE ADDRESS: ADDRESSEE: SEED AND BERRY STREET: 6300 Columbia Center CITY: Seattle STATE: Washington COUNTRY: USA ZIP: 98104 COMPUTER: EMPORABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: PARD BERRY SOFTWARE: PATENTIN BATA: APPLICATION DATA: APPLICATION NUMBER: 21,0392 RETERENCE, DOOK TELEFANION: NAME: Maki, David J. REGISTRATION NUMBER: 21 TELENOMINICATION INFORMATION: TELENOME: (206) 622-4900 TELENOME: CASS OF TELENOME: 21 TELENOME: ASS OF TELENOME: 21 TELENOME: CASS OF TELENOME: 21 TELENOME: ASS OF TELENOME: 21 TELENO	Query Ma Best Loc Matches
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APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROIL INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 445;
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APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Indels
SOFTWARE: · PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 82; DB 4;
Pred. No. 1.3e-09;
0; Mismatches 14
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Pred. No. 1.3e-09;
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                                                        APPLICATION NUMBER: US/08/723,142A
ETLING DATE: 01-0CT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
RECISTRATION NUMBER: 210121.426
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
SOFTWARE: FastSEQ for Windows Version 3.0
                                                  UMBER: US/08/723,142A
01-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/09528784A Patent No. 6451315 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 85, Application US/09528784A
Patent No. 6451315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 38:
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56.2%;
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match . 75.3%
Best Local Similarity 56.2%
Matches 18, Conservative
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Best Local Similarity 56.2'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY:
US-08-723-142A-38
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                                                                                                    Sequence 38 Application US/08990571
Patent No. 6214971
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
UNMER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
STREET: Washington
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
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Pred. No. 1.3e-09;
0; Mismatches 14
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 38, Application US/08723142A
Patent No. 6306396
GERERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND ME
TITLE OF INVENTION: AND TREATMENT OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
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COMPUTER READABLE FORM:
BEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
,OPERATING SYSTEM: PC-DOS/MS-
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56.2%;
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(206) 682-6031
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 445 amino acids TYPE: amino acid
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Best Local Similarity 56.29
Matches 18; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND
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US-08-723-142A-38
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US-08-990-571-38
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NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /note= "Residue can be either Pro
OTHER INFORMATION: or Ile"
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or Thr"
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or Arg"
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Release #1.0, Version #1.30
CURREWT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, DAVId J.
REGISTRATION NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION OF SECTION:
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LOCATION: 7
OTHER INFORMATION: /note-
OTHER INFORMATION: or Thr'
FEATURE:
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NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: /note-
OTHER INFORMATION: or Gly
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LOCATION: 23
OTHER INFORMATION: /note
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LOCATION: 3
OTHER INFORMATION: /note
OTHER INFORMATION: or As
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OTHER INFORMATION:
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LOCATION:
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Patent No. 6183976
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT:
Houghton, Raymond
APPLICANT:
Sleath, Paul R.
TITLE OF INVENTION:
COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Redds, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: McNeill, Paul R.
APPLICANT: McNeill, Paul R.
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
LENGTH: 1132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 75.9%; Score 82; DB 4; Length 1132; Best Local Similarity 56.2%; Pred. No. 3.8e-09; Matches 18; Conservative 0; Mismatches 14; Indels
                                                                                                                                                                                                                                                                                                                                                 Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                             14; Indels
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Best Local Similarity 56.2%; Pred. No. 2.1e-09;
Matches 18; Conservative 0; Mismatches 14
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FILE REFERENCE: 210121.426C4
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
LENGTH: 666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 87, Application US/09528784A Patent No. 6451315 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
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Washington
                                                                                                                                                                                                                      TYPE: PRT
; ORGANISM: Babesia
US-09-528-784A-85
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US-09-528-784A-87
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STREET: 63
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STATE:
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OTHER INFORMATION: /note= "Residue can be either Glu
OTHER INFORMATION: or Gly"
FEATURE:
NAME/KEV: Modified-site
LOCATION: 12
  OTHER INFORMATION: /note= "Residue can be either Pro OTHER INFORMATION: or Ile"
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or Arg"
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or Thr"
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                                                                                                OTHER INFORMATION: /note= "Residue can be either Lys OTHER INFORMATION: or Thr"
                                                                                                                                                                                                                                                                                               /note= "Residue can be either Lys
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or Ser"
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or Glu"
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or Ala"
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OTHER INFORMATION: /note-
OTHER INFORMATION: or Ser'
FEATURE:
NAME/KEY: Modified-site
LOCATION: 28
                                        FEATURE:
NAME/KEY: Modified-site
LOCATION: 7
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LOCATION: 26
OTHER INFORMATION: /note
OTHER INFORMATION: or Th
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OTHER INFORMATION:
OTHER INFORMATION:
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Best Local Similarity
Matches 32; Conserv
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Patent No. 6214971
GENERAL INFORMATION
GENERAL INFORMATION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. INVBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia.Center, 701 Fifth Avenue
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    /note= "Residue can be either Cys or Ser"
                                                                                                /note= "Residue can be either Asp
or Glu"
                                                                                                                                                                                               /note= "Residue can be either Glu
or Ala"
                                                                                                                                                                                                                                                                                     /note= "Residue can be either Cys or His"
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MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATUS SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/990,571
11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 amino acids
TYPE: amino acids
STRANDEDNESS:
                                                  NAME/KEY: Modified-site
LOCATION: 28
COTHER INFORMATION: /note-
OTHER INFORMATION: or Glu
FEATURE:
NAME/KEY: Modified-site
LOCATION: 29
OTHER INFORMATION: /note-
OTHER INFORMATION: or Ala"
                                                                                                                                                                                                                                                     NAME/KEY: Modified-site
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STREET: bac.
CITY: Seattle
THE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                     OTHER INFORMATION:
COTHER INFORMATION:
US-08-845-258-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 1 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UZIP: 98104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-990-571-39
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RESULT 9
US-08-723-142A-39
Sequence 39, Application US/08723142A
Sequence 39, Application US/08723142A
Patent No. 6306396
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION:
TITLE OF IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: Modified-site
LOCATION: 5
OTHER INFORMATION: /note= "Residue can be either Pro
OTHER INFORMATION: or lle"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Residue can be either Glu or Gly"
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or Asp"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Residue can be either Lys
or Asn"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
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APPLICATION DATA:

APPLICATION NUMBER: US/08/723,142A

FILING DATE: 01-0CT-1996

CLASSIFICATION: 536

ATTORNEY, AGENT INFORMATION:

NAME: Maki, David J.

REGISTRATION NUMBER: 31,392

REFERENCE/DOCKET NUMBER: 210121.426

TELECOMMINICATION INFORMATION:

TELEPHONE: (206) 622-4900
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TELEFAX: (206) 622-6031
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
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NAME/KEY: Modified-site
LOCATION: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 32 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND B
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OTHER INFORMATION:
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OTHER INFORMATION:
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STATE: Washington
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ZIP: 98104
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APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: SNOWEIL, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION FILE REPRESENCE: 210121.4264
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 32;
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/note= "Residue can be either Ile
or Arg"
                                                                                                  /note= "Residue can be either His or Tyr"
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or Glu"
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or Ala"
                                                                                                                                                                                                          /note= "Residue can be either Thr
or Pro"
                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Residue can be either Cys or Ser"
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or His"
                                                                                                                                                                                                                                                                                               /note= "Residue can be either or Thr"
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                                                                                 LOCATION: 18
OTHER INFORMATION: /note-
OTHER INFORMATION: or Tyr
FEATURE:
NAME/KEY: Modified-site
LOCATION: 23
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) LOCATION: 30
OTHER INFORMATION: /note
) OTHER INFORMATION: Or Hi
US-08-723-142A-39
                                                                                                                                                                                                                                                                  NAME/KEY: Modified-site
LOCATION: 26
OTHER INFORMATION: /note
OTHER INFORMATION: or Th
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                                                                Modified-site
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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FEATURE:
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                                             FEATURE:
NAME/KEY:
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LENGTH: 32
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ORGANISM: Babesia microti FEATURE:

TYPE: PRT

NAME/KEY: VARIANT LOCATION: (3)...(3)

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GENERAL INFORMATION:
APPLICANT: Read, Steven G. et al.
TITLE OF INTENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 4; Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                      PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 79; DB 4; Pred. No. 3.4e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches
                                                                                 FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David.J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
  PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 53, Application US/08990571 Patent No. 6214971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear _
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Babesia Microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.18;
56.28;
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                                                                                                                                                                                                                                                                                                                                     275 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 275 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (206)682-6031 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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APPLICANT: Reed, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION NUMBER OF SEQUENCE: 53
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: SEED AND BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          74.1%; Score 80; DB 4; Length 32; 100.0%; Pred. No. 1.9e-10; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (28)...(28)
OTHER INFORMATION: Xaa = Aspartic Acid or Glutamic Acid
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                        ION: (11)...(11)
INFORMATION: Xaa = Glutamic Acid or Glycine
INFORMATION: Xaa = Glycine or Aspartic Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (29)...(29)
OTHER INFORMATION: xaa = Glutamic Acid or Alanine
                                                                                                                                                                                                                                                                                                          ION: (14)...(14)
INFORMATION: Xaa = Glutamic Acid or Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION: (26)...(26)
OTHER INFORMATION: Xaa = Isoleucine or Threonine
                                                                                                                                                                                                                                                                                                                                                                       ON: (15)...(15)
INFORMATION: Xaa = Isoleucine or Arginine
                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: VARIANT
LOCATION: (18)...(18)
OTHER INFORMATION: Xaa - Histidine or Tyrosine
                                        LOCATION: (5)...(5)
OTHER INFORMATION: Xaa = Proline or Isoleucine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : LOCATION: (30)...(30)
; OTHER INFORMATION: Xaa = Cysteine or Histidine US-09-528-784A-39
                                                                                                                                                                                                                      LUCATION: (12)...(12)
OTHER INFORMATION: Xaa = Lysine or Asparagine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: (23)...(23)
OTHER INFORMATION: Xaa = Threonine or Proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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                                                                                                        ION: (7)...(7)
INFORMATION: Xaa = Lysine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: (27)...(27)

THER INFORMATION: Xaa = Cysteine or Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 53, Application US/08845258 Patent No. 6183976 GENERAL INFORMATION:
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MEDIUM TYPE: Floppy
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CITY: Seattle
STATE: Washingt
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                                                                                                                                                                                                                                                                                                                                  APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: MONEILL, Particia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C4
CURRENT APPLICATION NUMBER: US/09/528,784A
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FASTESQ for Windows Version 3.0
                                     Length 275;
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TITLE OF INVENTION: Substitutes for Modified Starch and
TITLE OF INVENTION: Latexes in Paper Manufacture
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0380
CURRENT PAPLICATION NUMBER: US/09/008,172
CURRENT FILING DATE: 1998-01-16
EARLIER APPLICATION NUMBER: 08/482,711
EARLIER FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 2
SOFTWARE: FESTEED for Windows Version 3.0
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                                                                          14; Indels
                                     Score 79; DB 4; I
Pred. No. 3.4e-09;
0; Mismatches 14;
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Pred. No. 3.4e-09;
0; Mismatches 14
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4; Mismatches
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                                                                                                                                                                                                                                        Sequence 53, Application US/09528784A Patent No. 6451315 GENERAL INFORMATION: APPLICANT: Reed, Steven G. APPLICANT: Lodes, Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-008-172-2
; Sequence 2, Application US/09008172
; Patent No. 6127602
; GENERAL INFORMATION:
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ORGANISM: Streptococcus mutans
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56.2%;
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                                     73.1%;
56.2%;
                                 Query Match 73.19
Best Local Similarity 56.29
Matches 18; Conservative
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Best Local Similarity 56.2<sup>3</sup>
Matches 18; Conservative
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ORGANISM: Babesia microti
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Matches 8; Conserv
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US-09-528-784A-53
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US-08-990-571-53
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LENGTH: 275
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                                                      GENERAL INFORMATION:
APPLICANT: Nichols, Scott E.
TITLE OF INVENTION: Substitutes for Modified Starches and
TITLE OF INVENTION: Latexes in Paper Manufacture
FILE REFERENCE: 0357CR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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                                                                                                                                                                                       CURRENT PELLICATION NUMBER: US/09/210,361
CURRENT FILING DATE: 1998-12-11
CURRENT FILING DATE: 1998-12-11
EARLIER APPLICATION NUMBER: 09/007,999
EARLIER FILING DATE: 1998-01-16
EARLIER FILING DATE: 1998-009,620
EARLIER PELLING DATE: 1998-01-20
EARLIER PELLICATION NUMBER: 09/009,620
EARLIER APPLICATION NUMBER: 09/009,620
EARLIER PELLING DATE: 1998-01-20
EARLIER FILING DATE: 1998-01-20
EARLIER FILING DATE: 1998-01-16
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Pred. No.
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Sequence 6, Application US/09210361
Patent No. 6284479
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Best Local Similarity 27.6
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Sequence 38, Appl
Sequence 211, App
Sequence 85, Appl
Sequence 144, App
Sequence 144, App
Sequence 144, App
Sequence 37, Appl
Sequence 39, Appl
Sequence 39, Appl
Sequence 53, Appl
Sequence 54, Appl
Sequence 56, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 58, Appl
Sequence 195, Appl
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/ cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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Perfect score:
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Sequence 199, App
Sequence 198, App
Sequence 193, App
Sequence 203, App11
Sequence 203, App11
Sequence 2, App11
Sequence 10, App1
Sequence 11455, App
Sequence 11617, App Sequence 1156, App Sequence 11617, App Sequence 11617, App Sequence 12664, App Sequence 12664, App Sequence 1156, Ap
             US-09-853-079-199

US-09-853-079-198

US-09-853-079-198

US-09-853-079-193

US-09-853-079-193

US-09-853-079-193

US-09-853-079-197

US-10-74-409-2

US-10-077-751-2

US-10-077-751-2

US-10-115-023-4

US-10-115-023-4

US-10-115-023-4

US-09-184-208-4

US-09-184-208-4

US-09-184-208-4

US-09-185-242-11455

US-09-185-242-11455

US-09-185-242-11455

US-10-108-605-113
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US-09-815-242-12664
US-09-815-242-13160
US-09-925-301-1156
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               Sequence 38, Application US/09286488

Patent No. US20020169136A1

GENERAL INFORMATION:

APPLICANT: Reed, Steven G.

APPLICANT: Lodes, Michael J.

APPLICANT: Houghton, Raymond L.

APPLICANT: Sleath, Paul R.

APPLICANT: Sleath, Paul R.

TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION

FILE REFERENCE: 210121.4263

CURRENT APPLICATION NUMBER: US/09/286,488

CURRENT FILING DATE: 1999-04-05

NUMBER OF SEQ ID NOS: 83

SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 445;
                                                                                                                                                                                          METHODS FOR THE DIAGNOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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Pred. No. 6.7e-09;
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.
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56.2%;
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Best Local Similarity 56.2
Matches 18; Conservative
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US-09-286-488-38
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US-09-853-079-38
US-09-286-488-38
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LENGTH: 445
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                                                                                                                                                                                                          Score 82; DB 9; 1
Pred. No. 7.2e-09;
0; Mismatches 14
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APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THI
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI
FILE REFERENCE: 210121.426C11
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SED ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
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Pred. No. 1e-08;
0; Mismatches 1
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CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FASELSEQ for Windows Version 3.0
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CURRENT FILING DATE: 2000-12-13
NUMBER OF SEG ID NOS: 144
SOSTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 85
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Sequence 85. Application US/09853079

; Publication No. US20030109689A1

; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lodes, Michael J.
Houghton, Raymond L.
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McNeill, Patricia D.
Homer, Mary
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Lodes, Michael J.
Houghton, Raymond L.
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McNeill, Patricia D.
Homer, Mary
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56.2%;
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Best Local Similarity 56.2%;
Matches 18; Conservative
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US-09-853-079-211
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Best Local Similarity
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                                                                                    SEQ ID NO 211
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                                                                                                                             TYPE: PRT
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APPLICANT:
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APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 445
          APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TERATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 21021.4266.079
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SED ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
SED ID NO 38
LENGTH: 445
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APPLICANT: Lodes, Michael J.
APPLICANT: Bleath, Paul R.
APPLICANT: MoNeill, Patricia D.
APPLICANT: Homer, Mary
APPLICANT: Homer, Mary
APPLICANT: Compounds and METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
FILLE REFERENCE: 210121.426C11
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6.7e-09;
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Pred. No. 6.7e-(
0; Mismatches
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Publication No. US20030109689A1
GENERAL INFORMATION:
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Houghton, Raymond L.
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McNeill, Patricia D.
Homer, Mary
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56.28;
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US-09-853-079-38
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US-09-737-178-38
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Homer, Mary
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Best Local Similarity
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Best Local Similarity
Matches 18; Conserv
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LENGTH: 445
                                                                                                                                                                                                                                  TYPE: PRT
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APPLICANT:
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APPLICANT:
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APPLICANT:
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APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Glost, Paul R.
APPLICANT: Slasth, Paul R.
APPLICANT: Homer, Mary
APPLICANT: Greater Mary
APPLICANT: Georist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C11
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
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APPLICANT: Houghton, Raymond L.
APPLICANT: Bleath, Paul R.
APPLICANT: MICHAEL B.
APPLICANT: MONEY, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.42669
Score 82; DB 10; Length 677;
Pred. No. 1e-08;
0; Mismatches 14; Indels
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Pred. No. 1.8e-08;
0; Mismatches 14
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Pred. No. 1.8e-08;
                                                                                                                931 GHDKINKNKSGNAGIKSYDTQTPQETSDAHEE 962
                                                                                     1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
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CURRENT FILING DATE: 2000-12-13
                                                                                                                                                                                                                                    Sequence 87, Application US/09853079 Publication No. US20030109689A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 87, Application US/09737178 Patent No. US20010029295A1
75.9%;
56.2%;
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56.2%;
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Best Local Similarity 56.2%;
Matches 18; Conservative
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Best Local Similarity 56.28
Matches 18; Conservative
                      Best Local Similarity 56.2
Matches 18; Conservative
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SOFTWARE: FastSEQ for
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US-09-853-079-87
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                                                                                                                                                                                              RESULT 9
US-09-853-079-87
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    Query Match
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APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Paul R.
APPLICANT: Homer, Mary
APPLICANT: Homer, Mary
APPLICANT: Homer, Mary
APPLICANT: Gorist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C9
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Houghton, Raymond L. APPLICANT: Sleath, Paul R. APPLICANT: Sleath, Paul R. APPLICANT: Moneill, Patricia D. APPLICANT: Honer, Mary APPLICANT: Honer, Mary APPLICANT: Honer, Mary APPLICANT: Secrist, Heather TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION FILE REFERENCE: 210121-42611
CUBRENT APPLICATION NUMBER: US/09/853,079
CUBRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                  Score 82; DB 10; Length 666;
Pred. No. 1e-08;
0; Mismatches 14; Indels
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Pred. No. 1e-08;
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                                                                                                                                                                                                                                                                                                                                           Sequence 144, Application US/09853079
Publication No. US20030109689A1
GENERAL INFORMATION:
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Lodes, Michael J.
Houghton, Raymond L.
Sleath, Paul R.
MCNeill, Patricia D.
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
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56.2%;
                                                                                                       75.9%;
56.2%;
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Best Local Similarity 56.29
Matches 18; Conservative
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Matches 18; Conservative
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APPLICANT: Reed, S
                 TYPE: PRT
ORGANISM: Babesia
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ORGANISM: Babesia
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US-09-737-178-144
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LENGTH: 666
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LENGTH: 677
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APPLICANT: Aleath, Paul R.
APPLICANT: Aleath, Paul R.
APPLICANT: Honder, Mary
APPLICANT: Honner, Mary
APPLICANT: Honner, Mary
TILLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: 21012.426C11
CURRENT RAPLICATION NUMBER: 201-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastEEQ for Windows Version 3.0
LENGTH: 32
                                                                                                                                                                                                                                 Length 32;
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100.0%; Pred. No. 1e-09;
tive 0; Mismatches 0;
NAME/KEY: VARIANT
LOCATION: (29)...(29)
OTHER INFORMATION: Xaa = Glutamic Acid or Alanine
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OTHER INFORMATION: Xaa = Glycine or Aspartic Acid
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OTHER INFORMATION: Xaa = Glutamic Acid or Glycine
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OTHER INFORMATION: Xaa = Glutamic Acid or Glycine
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OTHER INFORMATION: Xaa = Isoleucine or Arginine
                                                                               : NAME/KEY: VARIANT
; LOCATION: (30)...(30)
; OTHER INFORMATION: Xaa = Cysteine or Histidine US-09-286-488-39
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OTHER INFORMATION: Xaa = Proline or Isoleucine
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OTHER INFORMATION: Xaa = Lysine or Asparagine
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OTHER INFORMATION: Xaa = Lysine or Threonine
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Lodes, Michael J.
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ORGANISM: Babesia microti
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US-09-853-079-39
                                                                                                                                                                                                                                 Query Match
                                                                            FEATURE:
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Pred. No. 1.7e-08;
0; Mismatches 14; Indels
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APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION FILE REFERENCE: 210121.4263
CURRENT APPLICATION NUMBER: US/09/286,488
CURRENT FILING DATE: 1999-04-05
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                                         NAME/KEY: VARIANT
LOCATION: (14)...(14)
LOCATION: (14)...(14)
NAME/KEY: VARIANT
LOCATION: (15)...(15)
OTHER INFORMATION: Xaa = Isoleucine or Arginine
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LOCATION: (29)...(29)
OTHER INFORMATION: Xaa = Glutamic Acid or Alanine
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OTHER INFORMATION: Xaa = Isoleucine or Threonine
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                                                                                                                                                                           NAME/KEY: VARIANT
LOCATION: (18)...(18)
OTHER INFORMATION: Xaa = Histidine or Tyrosine
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: LOCATION: (30)...(30)
: OTHER INFORMATION: Xaa = Cysteine or Histidine
US-09-737-178-39
                                                                                                                                                                                                                                                                     LOCATION: (23)...(23)
OTHER INFORMATION: Xaa = Threonine or Proline
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                         OTHER INFORMATION: Xaa = Lysine or Asparagine
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OTHER INFORMATION: Xaa = Cysteine or Serine
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SOFTWARE: FastSEQ for Windows Version 3.0
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56.2%;
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Best Local Similarity 56.2
Matches 18; Conservative
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; ORGANISM: Babesia microti
US-09-286-488-53
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SEQ ID NO 53
LENGTH: 275
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US-09-286-488-53
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.42669
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
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o. 1e-09;
0; Indels
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OTHER INFORMATION: Xaa = Aspartic Acid or Glutamic Acid
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OTHER INFORMATION: Xaa = Glycine or Aspartic Acid
NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: VARIANT
LOCATION: (29)...(29)
OTHER INFORMATION: Xaa = Glutamic Acid or Alanine
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OTHER INFORMATION: Xaa = Glutamic Acid or Glycine
NAME/KEY: VARIANT
                                                                                                                                                      LOCATION: (26)...(26)
OTHER INFORMATION: Xaa = Isoleucine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCATION: (30)...(30) CTHER INFORMATION: Xaa - Cysteine or Histidine US-09-853-079-39
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OTHER INFORMATION: Xaa = Proline or Isoleucine
OTHER INFORMATION: Xaa = Histidine or Tyrosine
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                                                              LOCATION: (23)...(23)
OTHER INFORMATION: Xaa = Threonine or Proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LOCATION: (7)...(7)
OTHER INFORMATION: Xaa = Lysine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 74.1%; Score 80; DB Best Local Similarity 100.0%; Pred. No. 1e-Matches 32; Conservative 0; Mismatches
                                                                                                                                                                                                                                              LOCATION: (27)...(27)
OTHER INFORMATION: Xaa - Cysteine or Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 39, Application US/09737178 Patent No. US20010029295A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed, Steven G.
Lodes, Michael J.
Houghton, Raymond L.
Sleath, Paul R.
MONEILL, Patricia D.
Homer, Mary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: VARIANT LOCATION: (7)...(
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LENGTH: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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Search completed: July 16, 2003, 18:08:36 Job time : 6.2344 secs

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(without alignments)
814.396 Million cell updates/sec
                                                                                                                    July 16, 2003, 17:50:14; Search time 3.7774 Seconds
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                       108
1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                - protein search, using sw model
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                                                                                                                                                                                                                          score:
                                                                              OM protein
                                                                                                                                                                                                                       Perfect sc
Seguence:
                                                                                                                      Run on:
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BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	dextransucrase (EC	Ω		pseudouridine synt	hypothetical prote		д				_	Н	probable serine/th	glutamine-fructose	glutamine-fructose	hypothetical prote	hypothetical prote	⊆	Tbc1 protein - mou	cation efflux syst	¤	hypothetical prote	lipoprotein [impor	dehydrin-like prot		opacity protein op	hypothetical prote	conserved hypothet	IstA protein homol
SUMMARIES	ID	A45866	S19247	B69825	A82236	F64232	S59314	C84584	C86232	T23004	T45054	T28817	C72260	T01086	D64711	H71809	T21507	S54461	S64758	T29104	C96945	S14177	T52359	G90603	KNMUHY	T45729	S16286	T51571	A89782	A37801
	DB	7	7	7	7	-	7	7	7	7	7	7	7	7	7	7	7	7	7	7	~	7							7	
	Query Match Length	1431	1033	488	290	367	251	261	425	1227	82	292	368	492	597	597	618	096	1048	1141	1166	1250	1400	1546	127	127	201	327	370	431
dР	Query Match	36.1	35.6	35.2	34.3	34.3	33.3	32.4																					30.6	
	Score	(4)	38.5	38	37	37	36	35	32	35	34	34	34	34	34	34	34	34	34	34	34	34	34	34	33	33	33	33	33	33
	Result No.	1	7	ĸ	4	Ω	9	7	σο	Ø	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

A; Gene: FlyBase: Tk48D

. hypothetical prote	neurofilament trip	TTAGGG repeat-bind	hypothetical prote	hypothetical prote	transcription fact	hypothetical prote	hypothetical prote	triose-phosphate i	hypothetical prote	non intermediate f	hypothetical prote	late 33K protein -	hypothetical expor	insulin-like growt	N-acetylmuramoyl-L
					•	•									
A69745	QFMSL	869055	H84798	846833	A56199	T08991	G90064	S71595	G71362	T14462	T43439	S10212	F95955	A35037	C44816
7	Н	7	7	7	7	7	7	7	7	7	7	7	7	Н	7
483	543	562	571	605	802	1966	91	117	139	165	183	217	253	266	272
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30	30	30	30	30	30	30.6	29	29	29	29	29	29	29	29	29
33	33	33	33	33	33	33	32	32	32	32	32	32	32	32.	32
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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dextransucrase (EC 2.4.1.5) precursor - Streptococcus mutans
C;Species: Streptococcus mutans
C;Species: Streptococcus mutans
C;Accession: A45866
B;Honda, O.; Kato, C.; Kuramitsu, H.K.
J. Gen. Microbiol. 136, 2099-2105, 1990
A;Title: Nucleocitde sequence of the Streptococcus mutans gtfD gene encoding the gluco A;Reference number: A45866; MUID:91100958; PMID:2148600
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Pulido, D.; Campuzano, S.; Koda, T.; Modolell, J.; Barbacid, M.
EMBO J. 11, 391-404, 1992
A;Title: Dtrk, a Drosophila gene related to the trk family of neurotrophin receptors, A;Reference number: S19247; MUID:92164624; PMID:1371458
A;Accession: S19247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell adhesion protein Gp160-Dtrk - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 24-Sep-1999
C;Accession: S1247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1033 <PUL>
A;Cross_references: EMBL:X63453; NID:97883; PIDN:CAA45053.1; PID:97884
C;Genetics:
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Pred. No. 10;
4; Mismatches 1
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                                                                                                                                                                                                                                                                                                                                                <CP4>
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                                                                                                                                                                                                                               36.1%;
ilarity 27.6%;
Conservative 4
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Best Local Similarity
                                                                                                                                                                                                A; Molecule type: DNA
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S19247
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Gaps

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13; Indels

Length 290;

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hypothetical protein homolog MG295 - Mycoplasma genitalium C; Species: Mycoplasma genitalium 10. Sep-1999 #text_change 07-Dec-1999 (C; Accession: F64232 R; Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.M.; Furimann, J.; Nguyen, D.; Utterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, C.A.; Venter, J.C. Science 270, 397-403, 1995 Aritical The minimal gene complement of Mycoplasma genitalium. A; Reference number: A64200; MUID:96026346; PMID:7569993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R; Delius, H. submitted to the EMBL Data Library, June 1995
A; Description: 36.8 kb of S.cerevisiae chromosome XII including ACE2, CKII, PDC5, SLS A; Accession: S59313
A; Accession: S59314
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A;Residues: 1-251 <VER>
A;Cross-references: EMBL:273298; NID:91360532; PIDN:CAA97695.1; PID:e245566; PID:9136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:U39710; GB:L43967; NID:g1045989; PID:g1045993; TIGR:MG295 A;Experimental source: strain G-37 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA A;Residues: 1-367 <TIGR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein YLR126c - yeast (Saccharomyces cerevisiae)
N;Alternate names: hypothetical protein L3105
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisian
C;Date: 29-Nov-1995 #sequence_revision 23-Feb-1996 #text_change 19-Apr-2002
C;Accession: S59314; S64963; S64968; S69413
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A; Residues: 1-251 < DEL>
A; Residues: 1-251 < DEL>
A; Cross-references: EMBL:X91258; NID:9995686; PIDN:CAA62637.1; PID:9995688
A; Experimental source: strain S288C
B; Verhasselt, P.; Voet, M.; Volckaert, G.
submitted to the Protein Sequence Database, May 1996
A; Reference number: S64943
A; Accession: S64963
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34.3%; Score 37; DB 1; Length 367; llarity 70.0%; Pred. No. 6.9; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R.Delius, H.; Hebling, U.
submitted to the Protein Sequence Database, May 1996
A.Reference number: S64967
                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Genetic code: SGC3
C;Superfamily: probable membrane protein YDL033c
                                                                                                                                                      34.3%; Score 37; DB 36.4%; Pred. No. 5.4; Live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                   79 GHPPTRANRKSVANKKKNATQT 100
                                                                                                                                                                                                                                                                                                             1 GHXKXNXNKSXXAXXKSXDTQT 22
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                                                                                                                                                      Query Match
Best Local Similarity 36.4
Matches 8; Conservative
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Matches 7; Conserv
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                                              A;Gene: VC1140
A;Map position: 1
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               C; Genetics
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species: Bacillus subtliss
C; Species: Bacillus subtliss
C; Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C; Accession: B65825
C; Baco: 1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C; Accession: B65825
C; Brow, S; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chc
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A; Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler, ecch, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, R.; Ogiwara, A.; Oudega, B.; Rose, M.; Sadaie, Y.; Sado, T.; Scanlon, A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tamaka, T.; Tergerta, P.; Yasamoto, V.; Vohlyama, T.; Winters, P.; Winter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pseudouridine synthase family 1 protein VC1140 [imported] - Vibrio cholerae (strain N169 C;Species: Vibrio cholerae (strain N169 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001 R;Heldelberg. T.F. Free.
A;Cross-references: FlyBase:FBgn0004839
C;Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo
C;Keywords: ATP
F;690-1028/Domain: protein kinase homology <KIN>
F;698-706/Region: protein kinase ATP-binding motif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:299109; GB:AL009126; NID:92633260; PIDN:CAB12776.1; PID:e1182938;
A;Experimental source: strain 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-290 <HEI>
A;Cross-references: GB:AE004194; GB:AE003852; NID:g9655612; PIDN:AAF94299.1; GSPDB:GN001
A;Experimental source: serogroup 01; strain NI6961; biotype El Tor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RiHeidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, I. R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A.Fitle: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82236
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                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                             11; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cell wall-binding protein homolog yhdD - Bacillus subtilis
                                                                                                                                                                                                                                    DB 2;
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                                                                                                                                                                                                                                    Score 38.5; DI
Pred. No. 9.4;
                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 38; DB;
Pred. No. 5.6;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                             1 GHXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KSNSNKSSSSSSKSSNKS 166
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                                                                                                                                                                                                                                    35.6%;
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Best Local Similarity 36.89
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                             10; Conservative
                                                                                                                                                                                                                                                                   Sest Local Similarity
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C. Species: Caenorhabditis elegans
C. Species: Caenorhabditis elegans
C. Species: Caenorhabditis elegans
C. Date: 21-Jan-2000
Sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
C. Accession: T45054
C. Accession: T45054
R. Milson: Ruthor, L.; Gardner, A.; Green, P.; Hawkins, T.; Hillier, L.; Jier, M.; Jonature 368, 72-38, 1994
R.; O'Callaghan, M.; Parsons, J.; Percy, C.; Rifken, L.; Roopra, A.; Saunders, D. Nature 368, 32-38, 1994
R.; O'Callaghan, M.; Parsons, J.; Mohldman, P.
R.; Althors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E. A.; Authors: Shownkeen, R.; Mohldman, P.
R.; Altile: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans. A; Reference number: 843531; MUID:94150718; PMID:7906398
A; Accession: T45054
A; Accession: T45054
A; Mesidues: 1-82 CWILL.
A; Residues: 1-82 CW
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A;Introns: 31/3; 58/1; 279/3; 429/2; 544/3; 638/2; 801/2; 887/1; 929/2; 1025/3; 1062/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMEL:Z68005; PIDN:CAA91990.1; GSPDB:GN00028; CESP:F59F3.1 A;Experimental source: clone F59F3 C;Genetics:
A;Residues: 1-425 <STO>
A;Cross-references: GB:AE005172; NID:g2160172; PIDN:AAB60735.1; GSPDB:GN00141
C;Genetics:
A;Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein F59F3.1 - Caenorhabditis elegans .
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein Y39B6B.bb [imported] - Caenorhabditis elegans
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                                                                                                                                                                                   2; Length 425
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A, Status: preliminary; translated from GB/EMBL/DDBJ
A, Molecule type: DNA
A, Residues: 1-1227 <WILD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T23004
R;Kershaw, J.
submitted to the EMBL Data Library, November 1995
A;Refered to umber: 219651
                                                                                                                                                                               Score 35; DB 2
Pred. No. 21;
5; Mismatches
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Pred. No. 6.5;
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1050 GLSKKHTNKTYRTKKSKDT 1069
                                                                                                                                                                                                                                                                                                                                                                          197 NGNKKLDAAFRDAETKTLED 216
                                                                                                                                                                                                                                                                                                                                    6 NXNKSXXAXXKSXDTQTXQE 25
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37.5%;
                                                                                                                                                                                   32.4%;
30.0%;
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Best Local Similarity 37.5%;
Matches 9; Conservative
                                                                                                                                                                               Query Match 32.45
Best Local Similarity 30.05
Matches 6; Conservative
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A;Note: Y39B6B.bb
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C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C;Accession: C84584
R;Lin, X; Kaul, S; Rounsley, S.D; Shea, T.P; Benito, M.I.; Town, C.D.; Fujii, C.Y.; W.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Wanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. A;Itle: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: C86232
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizco, M.; Roneey, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, A;Authors: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719; PMID:11130712
                                                                                                                                                                                                                                                A.Molecule type: DNA
A.Residues: 1-251 <VEW>
A.Cross-references: EMBL:X89514; NID:g1297019; PIDN:CAA61704.1; PID:e198755; PID:g129704
                              A;Cross-references: EMBL:273298; NID:91360532; PIDN:CAA97695.1; PID:e245566; PID:9136053
A;Experimental source: strain 5288C
R;Verhasselt, P.; Volckaert, G.
submitted to the EMBL Data Library, September 1995
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A; Molecule type: DNA
A; Residues: 1-261 <STO>
A; Residues: 1-261 <STO>
C; Genetics: GB: AE002093; NID: 94580468; PIDN: AAD24392.1; GSPDB: GN00139
C; Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 2; Length 251;
Pred. No. 7.6;
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Pred. No.
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illarity 32.0%;
Conservative
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A; Map position: 12R
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Best Local Similarity 32...
The Conservative
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A; Accession: S69413
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Best Local Similarity
Matches 8; Conserv
A; Residues: 1-251 <DEW>
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A; Map position: 2
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Jutamine-fructose-6-phosphate transaminase (isomerizing) (EC 2.6.1.16) - Helicobacte NiAlternate names: glucosamine fructose-6-phosphate aminotransferase [misnomer] C: Species: Helicobacter pylori (c) Species: Helicobacter pylori (c) Species: Helicobacter pylori (c) Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 19-Jul-2002 (c) Accession: D64711 (c) Richardson, D.: Dodson, R.; Khalak, H.G.; Glodek, A.; McKe Son, J.D.; White, O.; Kerlavage, A.R.; Clayton, R.; Khalak, H.G.; Glodek, A.; McKe Son, J.D.; Kelley, J.M.; Cotton, M.D.; Weldman, J.M.; Fujii, C.; Bowman, C.; Watthey, Nature 388, 539-547, 1997 (c) M.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, A.Filer The complete genome sequence of the gastric pathogen Helicobacter pylori. A; Accession: D64711
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A; Variety: strain J99

A; Variety: strain J99

C; Accession: H71809

E; All R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.

E; All R.A.; Ling, L.S.L.; Moir, D.T.; King, B.L.; Brown, E.D.; Doig, P.C.; Smith, D.

Nature 397, 176-180, 1999
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A;Residues: 1-597 <ARN>
A;Cross-references: GB:AE001564; GB:AE001439; NID:g4156032; PIDN:AAD06999.1; PID:g415
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submitted to the EMBL Data Library, November 1998
A; Description: Sequence of A. thaliana BAC T10P11 from chromosome IV.
A; Reference number: 214248
A; Accession: T01086
A; Status: translated from GB/EMBL/DDBJ
A; Molecule type: DNA
A; Residues: 1-492 < KAP>
A; Cross-references: EMBL: AC002330; NID: 92262135; PID: 92262143
A; Experimental source: cultivar Columbia
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 492;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                      .;
?
                                                                                                                                                                                                                                                                                                                                                                                                                Score 34; DB 2
Pred. No. 39;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47 YRRSNKNKSLESSSKSNHT 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 HXKXNXNKSXXAXXKSXDT 20
                                                                                                                                                                                                                                                                                                                                                                                                                   31.5%;
36.8%;
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33.3%;
                                                                                                                                                                                                                                                                                                                        A;Note: T10P11.10
C;Keywords: phosphotransferase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity Matches 7; Conserv
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Best Local Similarity
Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: ll-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: C72260
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MUID:99287316; PMID:10360571
A;Accession: C72260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A:Cross-references: GB.AE001791; GB:AE000512; NID:94981929; PIDN:AAD36441.1; PID:9498193
A:Experimental source: strain MSB8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable serine/threonine-specific protein kinase (EC 2.7.1.-) T10P11.10 - Arabidopsis C; Species: Arabidopsis thaliana (mouse-ear cress)
C; Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 24-Mar-1999
C; Accession: T01086
R; Kaplan, N.; Johnson, D.; Schutz, K.; Gnoj, L.; Hoffman, J.; Till, S.; de la Bastide, hi, M.; Martienssen, R.; Chen, E.Y.; Wilson, R.; McCombie, W.R.
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A; Residues: 1-292 <FAV>
A; Residues: 1-292 <FAV>
A; Cross-references: EMBL:U50308; PIDN:AAC48005.1; GSPDB:GN00023; CESP:F07C3.5
A; Experimental source: strain Bristol N2; clone F07C3
A; Genetics:
A; Gene: CESP:F07C3.5
                                                                                                                                                                   hypothetical protein F07C3.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 29-Oct_1999 #sequence_revision 29-Oct-1999 #text_change 04-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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A;Introns: 54/1; 136/1; 160/3; 210/3; 283/3
C;Superfamily: Caenorhabditis elegans hypothetical protein F07C3.5
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C; Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #tex
C; Accession: 128817
R; Favello, A.; Gattung, S.
submitted to the EMBL Data Library, March 1996
A; Description: The sequence of C. elegans cosmid F07C3.
A; Reference number: 220528
A; Accession: T28817
A; Status: preliminary; translated from GB/EMBL/DDBJ
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4 KXNXNKSXXAXXKSXDTQTXQE 25
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Matches 7; Conserv
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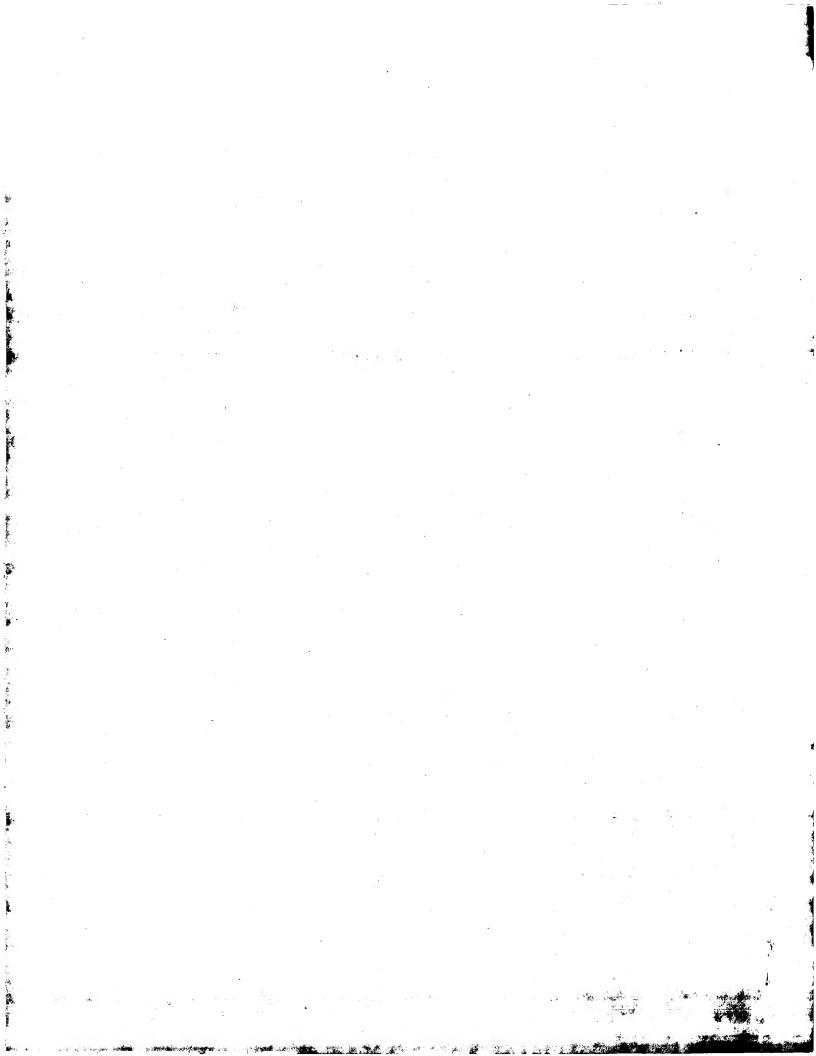
g

qq δ

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A, Experimental source: strain J99
C, Genetics:
A, Gene: glmS
C, Superfamily: glutamine-fructose-6-phosphate aminotransferase (isomerizing)
C, Keywords: aminotransferase, intramolecular oxidoreductase, isomerase
F; 2-597/Product: glutamine-fructose-6-phosphate transaminase (isomerizing) #status predifF; 2/Active site: Cys #status predicted
                                                                                                                                                                                                                                                                                                            Gaps
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31.5%; Score 34; DB 2; Length 597;
Best Local Similarity 33.3%; Pred. No. 47;
Matches 8; Conservative 3; Mismatches 13; Indels
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Search completed: July 16, 2003, 18:09:56 Job time: 5.7774 secs

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GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

July 16, 2003, 17:37:24; Search time 1.8887 Seconds (without alignments) 702.728 Million cell updates/sec Run on:

US-09-853-079-39 108 1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 segs, 41476328 residues Searched:

112892 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_40:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description		_		ß	ے	ဌ	S	P14771 saccharomyc				Sacc		_			P24808 bacillus su	P36103 saccharomyc		P17936 homo sapien	Q9y7t1 schizosacch		_		P40462 saccharomyc	_		P28569 saccharomyc	Q09624 caenorhabdi	_	O9pkz4 chlamydia m	Ġ	Q9zdi3 rickettsia
SUMMARIES	ΔI	GTFD	TRMU_MYCGE	PODX_MOUSE	TAT_SIVA1	GLMS_HELPJ	GLMS_HELPY	YMX6_YEAST	SC25_YEAST	DHX1_ARATH	T232_BACTB	NFL_MOUSE	TBF1_YEAST	APM2_YEAST	E2F_DROME	V33P_ADE41	IBP3_PIG	CWLA_BACSU		IBP3_BOVIN	IBP3_HUMAN	YCJ5_SCHPO	OSB1_HUMAN	OSB1_RABIT	CC53_YEAST	YIN7_YEAST	MY1B_DROME	NMD2_SCHPO	TRK1_SACBA	YS89_CAEEL	PBP2_HAEIN	SSB_CHLMU	RUVA_STRPY	RS4_RICPR
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	Length	1462	367	503	119	296	296	960	1253	128	431	542	295	605	802	217	266	272	277	291	291	323	807	808	812	946	1026	1049	1241	3178	651	160	198	202
dР	Query	36.1																				29.6											28.7	28.7
	Score	39	37	36	34	34	34	34	34	33	33	33	33	33	33	32	32	32	32	32	32	32	32	32	32	32	32	32	32	m		31	31	31
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		saccharomyc	saccharomyc	yersinia pe	chlamydia p	saccharomyc	arabidopsis		saccharomyc	escherichia	scherichia
P93000	091//1	P32772	P38763	982aw	09z798	P47018	P49966	075925	P33748	P58363	P22763
GL23_ARATH	HB/A_XENLA	UGX2_YEAST	YHI2_YEAST	YOG2_YERPE	Y808_CHLPN	YJM3_YEAST	SR52_ARATH	PIA1_HUMAN	MSN2_YEAST	ARCB_ECO57	ARCB_ECOLI
Η,	-		Н	H	7	П	~	Н	~	Н	7
219	220	223	256	366	444	478	495	651	704	778	778
28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7	28.7
31	31	31	31	31	31	31	31	31	31	31	31
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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RESULT 3
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MT4245).

D -> Y (IN STRAIN MT4251).

E -> K (IN STRAIN MT4251).

G -> IR (IN STRAIN MT4245).

G -> R (IN STRAIN MT4245).

G -> R (IN STRAIN MT4239).

Q -> H (IN STRAINS MT4239).

Y -> C (IN STRAINS MT4239).

Y -> C (IN STRAINS MT4239).

Y -> C (IN STRAINS MT4251).

Y -> C (IN STRAINS MT4245).

Y -> C (IN STRAINS MT4245).

Y -> C (IN STRAINS MT4245).

N -> D (IN STRAINS MT4245).

N -> D (IN STRAINS MT4245).

N -> D (IN STRAINS MT4245).

N -> G (IN STRAINS MT4245).

N -> C (IN STRAINS MT4239).

N -> C (IN STRAINS MT4467).
                                                                                                                                                                                                       STRAINS MT4239, MT4245, MT4251
                                                                                                                                                                                                                                                                                          N STRAIN MT4245).
N STRAINS MT4239 AND MT4251).
N STRAIN MT4239).
N STRAIN MT4239,
N STRAINS MT4239, MT4251 AND
                                                                                                                                            STRAIN MT4467).
STRAINS MT4239 AND MT4245).
STRAINS MT4251 AND MT8148).
STRAINS MT4239 AND MT4245 AND
STRAINS MT4239, MT4245 AND
                                                                                                                                                                                                                                           D -> N (IN STRAIN MT8148).
E -> D (IN STRAINS MT4239, MT4245 AND MT4251).
D -> N (IN STRAINS MT4239, MT4245 AND MT4251).
                                                                                                                                                                                                                                                                                                                                                    KKKYTQ -> EKEYTL (IN STRAIN MT4251).
A -> S (IN STRAIN MT4239).
TDQGSSC -> ADKGNDS (IN STRAIN MT4251)
TDQGSS -> ADKGN (IN STRAINS MT4239 AND
                                                                                    POTENTIAL.
GLUCOSYLTRANSFERASE-S.
3 x 63 AA APPROXIMATE TANDEM REPEATS.
                                                                             Glycosyltransferase; Signal; Repeat; Dental caries.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; Length 1462;
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W; 5C6541F0DCB0DF00 CRC64;
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| STRAIN MT4245).
| STRAIN MT4239).
| STRAIN MT8148).
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D -> N (IN S
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V -> F (IN S
F -> L (IN S
MT4467).
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AND MT8148)
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Pred. No.
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T -> I (I
A -> V (I
MT8148).
EMBL, D88656; BAA26107.1; --
EMBL, D88659; BAA26111.1; --
EMBL, D88662; BAA26112.1; --
EMBL, D89979; BAA26121.1; --
InterPro; IPR002479; CW_binding.
InterPro; IPR003318; GH_70.
Pfam; PF01473; CW_binding.1; 11.
Pfam; PF01324; Glyco_hydro_70; 1.
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27.6%;
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VARIANT
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                                                                                                                                                                                                                                                                                                                         STRAIN-ATCC 3353 / (G-37;
STRAIN-ATCC 3353 / (G-37;
STRAIN-B-66026346; PubMed=756993;
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J.M.,
Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S.,
Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
Frim Inimal gene complement of Mycoplasma genitalium.";
Science 270:397-403(1995).
I- CATALYTIC ACTIVITY: S-adenosyl-L-methionine + tRNA = S-adenosyl-L-homocysteine + tRNA containing 5-methylaminomethyl-2-
     ou-ocr-1996 (Rel. 34, Created)
01-ocr-1996 (Rel. 34, Last sequence update)
16-ocr-2001 (Rel. 40, Last annotation update)
Probable tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.161).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF03054; tRNA_Me_trans; 1.
TIGRAMS; TIGROUGYO; trmU; 1.
Transferase; Methyltransferase; tRNA processing; Complete proteome.
SEQUENCE 367 AA; 41887 MW; FRC6409D8C2D0625 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                    Mycoplasma genitalium.
Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB 1; Length 367, Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        thiouridylate.
-!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: BELONGS TO THE TRMU FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PODX_MOUSE STANDARD; PRT; 503 AA. 09R0M; 09ESL; 1, Created) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last senotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Podocallyxin-like protein 1 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
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InterPro; IPR004135; tRNA_Me_trans.
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MEDLINE=20057139; Pubmed=10591182;
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70.0%;
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Best Local Similarity 70.0.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                            NCBI_TaxID=2097;
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TRMU_MYCGE
P47537;
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Gaps

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17; Indels

4.2; Mismatches

Conservative

Best Local Similarity Matches 8; Conserv

3

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-:- SIMILARITY: CONTAINS 1 TYPE-2 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
   Olmstead R.A., Hirsch V.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=85963;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter
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                                                                                                                                                                                                         KENYA.
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Matches
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                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                    "Identification of podocalyxin-like protein 1 as a novel cell surface marker for hemangloblasts in the murine aorta-gonad-mesonephros
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                filtration pathway between neighboring foot processes in the podocyte by charge repulsion.
SUBCELDULAR LOCATION: Type I membrane protein (Potential).
TISSUE SPECIFICITY: (Johnstular epithelium cell (podocyte).
PTM: Sialoglycoprotein (By similarity).
SIMILARITY: BELONGS TO THE PODOCALXXIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                     FUNCTION: Functions as an antiadhesin that maintains an open
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MEDLINE-90156504; Pubmed-2304139;
Johnson P.R., Fomsgaard A., Allan J., Gravell M., London W.T.,
Copeland N.G., Jenkins N.A., Okabe M., Kogo H., Mukouyama Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36; DB 1; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Simian immunodeficiency virus (AGM155 isolate) (SIV-AGM).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15; Indels
                                                                                                                                           Kershaw D.B., Li J.;
"Gene structure of mouse podocalyxin.";
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     786A1ECF65484D1F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PODOCALYXIN-LIKE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transmembrane; Polymorphism.
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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(Rel. 23, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLCNAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
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26.9%;
                                                                                          [mmunity 11:567-578(1999)
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Matches 7; Conserv
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                                                                                                                              SEQUENCE FROM N.A.
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167
206
303
78
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CARBOHYD
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TAT_SIVA1
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MEDLINES-99120557; PubMed-9923682;
MEDLINES-99120557; PubMed-9923682;
Alm R.A., Ling L.-S.L., Moir D.T., King B.L., Brown E.D., Doig P.C.,
Smith D.R., Noonan B., Guild B.C., deJonge B.L., Carmel G.,
Tummino P.J., Caruso A., Uria-Nickelsen M., Mills D.M., Ives C.,
Gibson R., Merberg D., Mills S.D., Jiang Q., Taylor D.E., Vovis G.F.,
Trust F.J.;
                            unusual genetic diversity.";
J. Virol. 64:1086-1092(1990).
-!- FUNCTION: TRANSCRIPTIONAL REGULATOR THAT ACTS BY BINDING TO THE TRANS.ACTIVARING RESPONSIVE SEQUENCE (TAR) RNA ELEMENT AND ACTIVATES TRANSCRIPTION INITIATION AND/OR ELONGATION FROM THE LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SUBCELLUIAR LOCATION: Cytoplasmic (By similarity).
-!- SIMILARITY: IN THE C-TERMINAL SECTION; BELONGS TO THE SIS FAMILY.
GFAT SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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CATALYTIC ACTIVITY: L-glutamine + D-fructose 6-phosphate = L-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Genomic sequence comparison of two unrelated isolates of the human
Simian immunodeficiency viruses from African green monkeys display
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Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ranscription regulation; Activator; RNA-binding; Nuclear protein;
                                                                                                                                                                                                                                                                     -!- SUBUNIT: BINDS CYCLIN T1 (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: Nuclear; nucleolar.
-!- MISCELLANEOUS: THE 155 ISOLATE IS FROM A MONKEY IMPORTED FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -! - FUNCTION: CATALYZES THE FIRST STEP IN HEXOSAMINE METABOLISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 AA; 13648 MW; 958DB1A3F7027729 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31.5%; Score 34; DB 1; 41.2%; Pred. No. 3.5;
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15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      596 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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Pfam; PF00539; Tat; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M29975; AAA91909.1; -
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Best Local Similarity
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                      between the Swiss Institute of Bloinformatics and the EMBL outstation. The European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000 (Rel. 39, Last sequence update)
15-JUV-2002 (Rel. 41, Last annotation update)
Glucosamine--fructose-6-phosphate aminotransferase [isomerizing]
(EC 2.6.1.16) (Hexosephosphate aminotransferase) (D-fructose-6-phosphate amidotransferase) (GFAT) (L-glutamine-D-fructose-6-phosphate amidotransferase) (Glucosamine-6-phosphate synthase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Definition 3. All C. (No.25.)

MEDLINE-9734467; PubMed-9222185;

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,

Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Dougherty B.A.,

Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,

Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,

McKenney K., Fitzderaid L.M., Lee N., Adams M.D., Hickey E.K.,

Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,

Cotton M.D., Weidman J.M., Eujii C., Bowman C., Watthey L., Wallin E.,

Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                   GATASE (BY SIMILARITY).
ISOMBRIZATION FRU-6P (BY SIMILARITY).
GLUTAMINE AMIDOTRANSFERASE.
C438BCCE6A245C28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Helicobacter pylori (Campylobacter pylori).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complete genome sequence of the gastric pathogen Helicobacter
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                                                                                                                                                                            Pfam; PF01380; SIS; 2.
TIGRAMS, TIGROLIS; GIMS; 1.
PROSITE; PS00443; GATASE_IYPE_II; 1.
Transferase; Aminotransferase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                   DB 1; Length 596;
                                                                                                                                                                                                                                                                                                                                            13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          596 AA
                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                          BY SIMILARITY
                                                                                                                                                                                                                                                                                                                   Score 34;
                                                                                                                                                                                                                                                                                                                                8
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                                                                                                                                                                                                                                                                                                                                                                   2 HXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                Pred
                                                                                                                                     InterPro; IPR000583; GATase_2.
InterPro; IPR001347; SIS.
                                                                                                               EMBL; AE001564; AAD06999.1; -.
                                                                                                                                                                                                                                                                                         66926 MW;
                                                                                                                                                                                                                                                                                                                  31.5%;
                                                                                                                                                              Pfam; PF00310; GATase_2; 1. Pfam; PF01380; SIS; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=26695 / ATCC 700392;
                                                                                                                                                                                                                                                                                                                                           8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                          596 AA;
                                                                                                                             1600
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Best Local Similarity
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                                                                                                                                                                                                                                                                 591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Helicobacter.
NCBI_TaxID=210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GLMS OR HP1532
                                                                                                                           HSSP; P17169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GLMS_HELPY
026060:
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ACT_SITE
DOMAIN
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SIMILARITY: CONTAINS 1 TYPE-2 GLUTAMINE AMIDOTRANSFERASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GATASE (BY SIMILARITY).
ISOMERIZATION FRU-6P (BY SIMILARITY).
GLUTAMINE AMIDOTRANSFERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID-4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 105.9 kDa protein in ADH3-RCA1 intergenic region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGRPAMS; TIGRO1135; glms; 1.
PROSITE; PS00443; GATASE_TYPE_II; 1.
Transferase; Aminotransferase; Glutamine amidotransferase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               31.5%; Score 34; DB 1; Length 596; 33.3%; Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 1; Length 960;
Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gentles S., Bowman S., Barrell B.G., Rajandream M.A., Submitted (MAY-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein.
SEQUENCE 960 Aa; 105873 MW; 05A4FA27129DB09B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       089C534BB85AD3F1 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 18;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      325 HFKSNPNELFIAISQSGETADTLE 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 HXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                     EMBL; AE000651; AAD08570.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000583; GATase_2.
InterPro; IPR001347; SIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       66939 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00310; GATase_2; 1. Pfam; PF01380; SIS; 2.
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hes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                MEROPS; C44.971;
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Q04279;
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ACT_SITE
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SH3 domain.
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SEQUENCE
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  Gaps
                                                                                                                                                                                                                                                                                                                            Damak F., Boy-Marcotte E., le Roscouet D., Guilbaud R., Jacquet M., "SDC25, a CDC25-like gene which contains a RAS-activating domain and
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                Saccharomyces cerevisiae (Baker's yeast).
Bukaryota; Fungi; Ascomycota; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales; Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Boy-Marcotte E., Damak F., Camonis J., Garreau H., Jacquet M., "The C-terminal part of a gene partially homologous to CDC 25 compresses the cdc25-5 mutation in Saccharomyces cerevisiae."; Gene 77:21-30(1989)
17; Indels
                                                                                                                                                                                                                                                                                                                                                       is a dispensable gene of Saccharomyces cerevisiae."; Mol. Cell. Biol. 11:202-212(1991).
                                                                                                                                             01-APR-1990 (Rel. 14, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
SCD25 protein.
SCD25 OR SDC25 OR YLL016W.
                                                                                                                       1253 AA.
1; Mismatches
                                                    438 NGNKNLENDITSSPTODLDEKSRSIEE 464
                         6 NXNKSXXAXXKSXDTQTXQEXXXXXEE
                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; S14177; S14177.
SGD; S0003939; SDC25.
InterPro; IPR000651; RasGEFN.
InterPro; IPR001895; RasGRF_CDC25.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-91156312; PubMed-2000228;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-90260633; PubMed-2188363;
                                                                                                                                                                                                                                                                                                             MEDLINE=91094833; PubMed=1986220;
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 668-1253 FROM N.A.
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 Conservative
                                                                                                                     STANDARD;
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Pfam; PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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6
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P14771;
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Salanoubat M., Lemcke M., Rieger M., Ansorge W., Unseld M.,
Rathmann B., Valle G., Bloecker H., Perez-Alonso M., Obermaier B.,
De Simone V., Choisne N., Artiguenave F., Robert C., Brottier P.,
Mincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
Schaefer M., Muellar-Auer S., Gabel C., Fucchs M., Benes V.,
Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangart S.,
Midelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
Navarro P., Chanscher K., Kauer G., Lochhert T.-H., Nordsiek G.,
Reichelt J., Scharfe M., Schoen O., Bargues M., Terol J., Climent J.,
Navarro P., Collado C., Perez-Perez A., Ottenwaelder B.,
Monarro P., Collado C., Perez-Perez A., Ottenwaelder B.,
Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccarla P., Mewes H.-W.,
Mayer K.F.X., Kaul S., Town C.D., Roo H.L., Tallon L.J., Jenkins J.,
Rooney T., Rizzo M., Walts A., Utterback T., Fujil C.Y., Shea T.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                            PROSITE; PS00720; GDS_CDC25; 1.
PROSITE; PS50002; SH3; 1.
Guanine-nucleotide releasing factor; Cell cycle; Cell division;
                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDILINE=92322990; PubMed=1633199;
Rouse D.T., Gehring C.A., Parish R.W.;
"Structure and sequence of a dehydrin-like gene in Arabidopsis
                                                                                                                                                                                                                                 DVVVKFI -> V (IN STRAIN 0L136).
MW; 2DE2C9EC27E3E60D CRC64;
                                                                                                                                                                                                                                                                                            Length 1253;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=cv. Landsberg erecta;
Rouse D.T., Heazlewood J.L.;
Submitted (JAN-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DHX1_ARATH STANDARD; PRT; 128 AA. P25863; QS50A7; Created) 01-MAY-1992 (Rel. 32, Created) 01-NOV-1995 (Rel. 32, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) ABRO1 OR DHNX OR AT3G50980 OR F24M12.20.
                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                            Score 34;
                                                                                                                                                                                           POLY-ASN.
POLY-ARG.
                                                                                                                                                                                                                                                                                                              Pred. No
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-cv. Columbia;
MEDLINE=21016720; PubMed=11130713;
                                                                                                                                                                                                                                                                                                                                                                                                           1208 NSNSNNKSQEKSRDDQTDE 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plant Mol. Biol. 19:531-532(1992)
                                                                                                                                                                                                                                                                                                                                                                    24
                                                                                                                                                                                                                                                                                                                                3;
                                                                                                                                                                                                                                                                                                                                                                      6 NXNKSXXAXXKSXDTQTXQ
                                                                                                                                                                                                                                                                                          31.5%;
36.8%;
                                                                                                                                                                                                                                                     144979
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Landsberg erecta;
Pfam; PF00617; RasGEF; 1.
Pfam; PF00618; RasGEFN; 1.
SMART; SM00147; RasGEF; 1.
SMART; SM00229; RasGEFN; 1.
                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                         26
74
434
434
584
593
1253 AA;
                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                              SM00326;
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SEQUENCE OF 1-27 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-Brain;
                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NEFL OR NFL.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NFL_MOUSE
P08551;
                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                    DNA BIND
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
NFL_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., Van Aken S., Pai G., Militscher J., Sellers P., Gill J.E., Feldblyum T.V., Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C., Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asamizu E., Sasamoto S., Kimura T., Idasawa K., Kawashina K., Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shinpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M., Tabata S., Saquence and analysis of chromosome 3 of the plant Arabidopsis thaliana."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                drought stress.
-!- SIMILARITY: BELONGS TO THE PLANT DEHYDRIN FAMILY.
-!- CAUTION: Ref.3 sequence differs from that shown due to erroneous
                                                                                                                                                              STRAIN=cv. Landsberg erecta; TISSUE-Leat;
MEDLINE=95035985; PubMed=7948863;
Welin B.V., Olson A., Nylander M., Palva E.T.;
"Characterization and differential expression of dhn/lea/rab-like genes during cold acclimation and drought stress in Arabidopsis
                                                                                                                                                                                                                            thaliana.";
Plant Mol. Biol. 26:131-144(1994).
-!- INDUCFION: Not induced by low temperature, abscisic acid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacillus thuringiensis (subsp. berliner).
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
NCBI_TaxID=1434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ARG/LYS-RICH (BASIC).
HIS/LYS-RICH (BASIC).
MISSING (IN REF. 1).
983558C3E18E31F4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Transposase for inscrtion sequence element IS232.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             431 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 6;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30.6%; Score 33; 31.8%; Pred. No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SER-RICH
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U19537; AAB00375.1; -.
EMBL; AL132980; CAB62620.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GHHDSNKTSSLGSTTTAYDTGT 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GHXKXNXNKSXXAXXKSXDTQT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN-1715;
MEDLINE-91072212; Pubmed-2174857;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00257; dehydrin; 1.
PROSITE; PS00315; DEHYDRIN_1; 1.
PROSITE; PS00823; DEHYDRIN_2; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000167; Dehydrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13435 MW;
                                                                                                                                                                                                                                                                                                       gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dehydrin; Multigene family
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; X64199; CAA45524.1;
                                                                                                                             Nature 408:820-822(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S22485; KNMUHY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 7; Conserv
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099335;
                                                                                                                                                     INDUCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transposition; DNA-binding; DNA recombination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Brain;

BELLINE-84158637; PubMed-3103856;

Julien J.-P., Meyer D., Flavell D., Hurst J., Grosveld F.;

"Cloning and developmental expression of the murine neurofilament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87064433; PubMed-3785173;
Lewis S.A., Cowan N.J.;
"Anomalous placement of introns in a member of the intermediate
filament multigene family: an evolutionary conundrum.";
Mol. Cell. Biol. 6:1529-1534(1986).
Menou G., Mahillon J., Lecadet M.-M., Lereclus D.; "Structural and genetic organization of IS232, a new insertion sequence of Bacillus thuringlensis."; J. Bacteriol. 172:6699-6696(1990).
-i- FUNCTION: INVOLVED IN THE TRANSPOSITION OF THE INSERTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-AUG-1988 (Rel. 08, Created)
01-OCT-1993 (Rel. 27, Last sequence update)
16-OCT-2001 (Rel. 40, Last amotation update)
Neurofilament triplet L protein (68 kDa neurofilament protein)
(Neurofilament light polypeptide) (NF-L).
                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE IS21/IS408/IS1162 FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lewis S.A., Cowan N.J.;
"Genetics, evolution, and expression of the 68,000-mol-wt neurofilament protein: isolation of a cloned cDNA probe."; J. Cell Biol. 100:843-850(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35 54 H-T-H MOTIF (POTENTIAL).
431 AA; 49893 MW; 3FB218504A50767A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 33; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               542 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 GHXKXNXNKSXXAXXKSXDTQT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27 GNLKMKINKSQLARELNVDRRT 48
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene family.";
Brain Res. 387:243-250(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M38370; AAA98140.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30.6%;
36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR001584; Rve. Pfam; PF00665; rve; 1. Transposable element; Tran
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Wouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                TRANSPOSASES.
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RESULT 12
TBF1_YEAST
                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation - the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                     J. BIOL. Chem. 265:19786-19791(1990).

-!- FUNCTION: NEUROPFILAMENTS USUALLY CONTAIN THREE IF PROTEINS: L, M, AND H WHICH ARE INVOLVED IN THE MAINTENANCE OF NEURONAL CALIBER.
-!- DOMAIN: THE EXTRA MASS AND HIGH CHARGE DENSITY THAT DISTINGUISH THE NEUROFILAMENT PROTEINS FROM ALL OTHER INTERMEDIATE FILAMENT PROTEINS REGUL OTHER TAILPIECE EXTENSIONS. THIS REGION MAY FORM A CHARGED SCAFFOLDING STRUCTURE SUITABLE FOR INTERACTION WITH OTHER NEURONAL COMPONENTS OR IONS.
-!- MISCELLANEOUS: NF-L IS THE MOST ABUNDANT OF THE THREE NEUROPALAMENT PROTEINS AND, AS THE OTHER NOMPOPLIMELIAL
INTERMEDIATE FILAMENT PROTEINS, IT CAN FORM HOMOPOLYMERIC 10-NM
                                             "Structure of the 68-kDa neurofilament gene and regulation of its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O-LINKED (GLCNAC) (BY SIMILARITY).
O-LINKED (GLCNAC) (BY SIMILARITY).
EPITOPE (RECOGNIZED BY IF-SPECIFIC
                                                                                                                                                                                                                                                              SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
              Nakahira K., Ikenaka K., Wada K., Tamura T.A., Furuichi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1; Length 542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Intermediate filament; Coiled coil; Neurone; Glycoprotein. INIT_MET 0 \\ 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TAIL, SUBDOMAIN B (ACIDIC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> I (IN REF. 1).
8EE9B8C6F0831D8C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MONOCLONAL ANTIBODY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Y -> S (IN REF. 1).
Y -> I (IN REF. 1).
M -> K (IN REF. 1).
V -> K (IN REF. 1).
D -> H (IN REF. 2).
R -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TAIL, SUBDOMAIN A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MISSING (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 27;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30.6%; Score 33; ilarity 25.0%; Pred. No. 2 Conservative 5; Mismatch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COIL 1B.
LINKER 12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COIL 2A.
LINKER 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LINKER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COIL 1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COIL 2B.
 PubMed-2246261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61448 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X02165; CAB51616.1; -. EMBL; M20480; AAA39814.1; -. EMBL; M13016; AAA39810.1; -. EMBL; M55423; AAA39812.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A25227; QFMSL.
MGD; MGI:97313; Nfl.
InterPro; IPR001664; IF.
PFam; PF00038; filament; 1.
PROSITE; PS00226; IF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   194
202
239
542 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
MEDLINE-91060592;
                            Mikoshiba K.;
                                                                                                                                                                                                                                                 FILAMENTS
                                                           expression.";
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CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
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SEQUENCE FROM N.A.

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STRAIN=S288c / AB972;

MEDIINE=97313271; pubMed=9169875;

MEDIINE=97313271; pubMed=9169875;

Araujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,

Araujo R., Aparicio A., Barcker M., Carpenter J., Cherry J.M.,

Chung E., Churcher C.M., Coster F., Davis R., Davis R.W.,

Duccan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,

Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,

A Hall J., Hebling W., Howmann R., Johnston M., Kalman S., Kleine K.,

A Marathe R., Mesgenguy F., Mewes H.-W., Mirtipati S., Moestl D.,

A Marathe R., Mesgenguy F., Mewes H.-W., Mirtipati S., Moestl D.,

A Marathe R., Johnston M., Schafer M., Schafer M., Schafer M., Schafer M., Schafer D., Petel F.X., Pohl T.M., Purnelle D., Schafer M., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration
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or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                              Brigati C., Kurtz S., Balderes D., Vidali G., Shore D.M.;
"An essential yeast gene encoding a TTAGGG repeat-binding protein.";
Mol. Cell. Biol. 13:1306-1314(1993).
                                                                                                                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                       01-0CT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
TBF1 protein (TTAGGG repeat-binding factor 1) (TBF alpha).
TBF1 OR YPL128C OR LPI16C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Iranscription regulation; Cell cycle; Nuclear protein;
Chromosomal protein; Telomere; DNA-binding.
                                                                                                                                                                                                                                Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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DAA -> ERR (IN REF. 1).
562 AA.
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PIR; A48079; A48079.
HSSP, P54274; 1BA5.
TEANSFAC; T01246; -
SGD; S0006049; TBF1.
PF6m; PF00249; myb_DNA-binding; 1.
PROSITE; PS00035; SANT; 1.
PROSITE; PS00037; NYB_1; 1.
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                                               01-JUL-1993 (Rel. 26, Created)
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  STANDARD;
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                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
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  TBF1_YEAST
Q02457;
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                                                                    ö
                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Dover J., Du Z., Favello A., Fulton L., Gattung S., Geisel C., Kirsten J., Kucaba T., Hilier L., Jier M., Johnston L., Langston Y., Latreille P., Louis E.J., Marri C., Mardis E., Menezes S., Mouser L., Nhan M., Rifkin L., Riles L., St Peter H., Trevaskis E., Vaughan K., Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A late Golgi sorting function for Saccharomyces cerevisiae Apmlp, but not for Apm2p, a second yeast clathrin AP medium chain-related
                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetales;
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                                   Length 562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.6%; Score 33; DB 1; Length 605; 31.8%; Pred. No. 30;
62823 MW; 2340F086468EC54F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          605 AA; 69990 MW; 7E216B11325EEE3C CRC64;
                                   DB 1;
                                                                                                                                                                                                                              ul-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN -2002 (Rel. 41, Last annotation update)
Adaptin medium chain homolog APM2.
                                                                                                                                                                                                                       605 AA
                                                                  1; Mismatches
                                                  28;
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                                   Score 33;
Pred. No.
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Pfam; PF00928; Adap_comp_sub; 1.
PROSITE; PS00990; CLAT_ADAPTOR_M_1; 1.
PROSITE; PS00991; CLAT_ADAPTOR_M_2; 1.
                                                                                                                                                                                                                       PRT;
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MEDLINE=94378003; PubMed=8091229;
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-S288C / REE526;
MEDLINE-95268148; PubMed-7749194;
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.. Biol. Cell 6:41-58(1995)
                                 30.6%;
53.8%;
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                                                                                                                         | : |||| ||
516 AASATEDTQTHQE 528
                                                                                                    13 AXXKSXDTQTXQE 25
                                                                    Conservative
                                                                                                                                                                                                                       STANDARD;
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562 AA;
                                                 Best_Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A
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SEQUENCE
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P38700;
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Mol. Biol
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13;

Mismatches

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RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA George R.A., Lewis S.E., Fichards S. Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandaell M.D., Zhang Q., Chen L.X.,
Ra Brandon R.C., Bogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxer E.G., Helt G., Nelson C.R., Milklos G.L.G.,
RA Abril J.F., Agbayani A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beson K.Y., Bencos P.V., Berman B.P., Bhanddari D., Botther P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Daviel S., M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabriellian A.E., Garraz C., Ferriacs S., Fleischmann W.,
RA Fosler C., Gabriellian A.E., Garraz C., Ferriacs S., Fleischmann R.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.K., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei W., Murphy B., Murphy L., Morris J., Mosherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Nelson K., Nixon K., Nusskenn D.R., Paceled J.M.,
Respectively R. Respectively R. Rasker D. P., Paceled J.M.,
Respectively R. Respectively R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dyson N.;
Drosophila E2F and DP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94158833; Pubmed-8114698;
Ohtani K., Nevins J.R.;
"Functional properties of a Drosophila homolog of the E2F1 gene.";
Mol. Cell. Biol: 14:163
                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoos, Arthropda; Mandibulata; Pancrustacea; Hexapo,
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                roc. Natl. Acad. Sci. U.S.A. 91:6359-6363(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=94294381; PubMed=8022787;
Dynlacht B.D., Brook A., Dembski M., Yenush L.,
"DNA-binding and trans-activation properties of
                                                                                                                                          E2F_DROME STANDARD; PRT; 805 AA. 027368; 077035; 10-100V-1997 (Rel. 35, Created) 16-0CT-2001 (Rel. 40, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) E2F OR E2F1 OR CG6376.
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|GHREHSTNKSSQYNSDEDDPNT 497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               melanogaster.";
Mol. Cell. Biol. 19:547-555(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Eye imaginal disk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spiez E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodsey T., Worley K.C., Wu D., Yang S., Yao Q.A., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng I., Zhong X.H., Zhong F.N., Zhou X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                         Royzman I., Whittaker A.J., Orr-Weaver T.L.; "Mutations in Drosophila DP and E2F distinguish G1-S progression from an associated transcriptional program."; Genes Dev. 11:1999-2011(1997).
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MEDLINE=96087653; PubMed=8537434;
Hao X.F., Alphey L., Bandara L.R., Lam E.W., Glover D.,
La Thangue N.B.;
"Functional conservation of the cell cycle-regulating transcription factor DRTFI/E2F and its pathway of control in Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Duronio R.J., Bonnette P.C., O'Farrell P.H.;
"Mutations of the Drosophila dDP, dE2F, and cyclin E genes reveal
distinct roles for the E2F-DP transcription factor and cyclin E
during the G1-S translion.";
Mol. Cell. Biol. 18:141-151(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DEVELOPMENTAL STAGE: Throughout embryonic development. SIMILARITY: BELONGS TO THE E2F/DP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRANSFAC; T01547; -.
FlyBase; FBgn0011766; E2f.
InterPro; IPR003316; E2F_TDP.
Pfam; PF02319; E2F_TDP; I.
Transcript.on regulation; DNA-binding; Nuclear protein;
Developmental protein; Activator.
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GLY-RICH.
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                                                                                                                                                                                                                                                                                                                    MEDLINE-98078671; PubMed-9418862;
                                                                                                                                                                                                          MEDLINE-97415323; PubMed-9271122;
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EMBL; U10184; AAA19003.1; -.
EMBL; AB011613; BAA32746.1; -.
EMBL; AE003735; AAF55904.1; -.
HSSP; Q16254; ICF7.
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Pieniazek N.J., Velarde J. Jr., Pieniazek D., Luftig R.B.;
"Nucleotide sequence of human enteric adenovirus type 41 hexon-
associated protein VIII precursor (PVIII) including the early region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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P19416; 064818;
P19416; 064818;
01-NOV-1990 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 21, Last annotation update)
33 Kba phosphoprotelin.
Human adenovirus type 41.
Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
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MEDLINE-90272433; PubMed-2349115;
Slemenda S.B., Pieniazek N.J., Velarde J. Jr., Pieniazek D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.6%; Score 32; DB 1; Length 217; 36.0%; Pred. No. 17; ive 1; Mismatches 15; Indels
                                                                                                                   DB 1; Length 805;
                                                                                                                                                11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X1313', 201851.
PIR; S04851; S04851.
PIR; S10212: S10212.
Late protein; Phosphorylation.
Late protein; Phosphorylation.
217 Aa; 24740 MW; B6ECDA6B3C24EC3E CRC64;
                                                      POLY-GLY.
H -> Q (IN REF. 1 AND 2).
BD49C813DDB2A77D CRC64;
                                                                                                                                                2; Mismatches
                                                                                                                               41;
                                                                                                                 30.6%; Score 33; 35.0%; Pred. No. 4
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               .GLY-RICH.
POLY-GLN.
POLY-ALA.
   POLY - SER
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                                                                                                                                                                           6 NXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                             13 NSNSSSSHTTTSSNTQRHQQ 32
                                                                                      87460 MW;
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Best Local Similarity 36.00
For 9; Conservative
                                                                                                                                 Local Similarity 35.09 tes 7; Conservative
249
573
533
601
710
245
519
525
594
701
127
805 AA;
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                                                                        CONFLICT
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ó;
                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pteryyota; Neotera: Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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MEDIJNE-98135459; PubMed-9475118;
Drew P.D., Gado A.M., Canning R.D., Nagle J.W., Dehejia A.M.,
Polymeropoulos M.H., Biddison W.E., Jacobson S., Becker K.G.;
"C2H7-546: a zinc finger protein differentially expressed in HTLV-1
infected T.C. Cells.":
                                                                                                                                                               STRAIN=BERKELEY;
Stapteton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
George R., Gonzalez M., Guarin H., Krommiller B., Li D., Liao G.,
Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S.,
Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
Celniker S.,
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SMART; SW00355; Znf_CZH2; 7.
PROSITE; PS000028; ZINC_FINGER_CZH2_1; 6.
PROSITE; PS50157; ZINC_FINGER_CZH2_2; 7.
Hypothetical protein; DNA-binding; Metal-binding; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                               Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AY071126; AAL48748.1; -- SEQUENCE 198 AA; 22012 MW; CE33F831FAB79D49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
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01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
21nc finger protein (Hypothetical 31.0 kDa protein).
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
RE17222p.
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50.0%; Pred. No. 48;
Live 5; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     4; Mismatches
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EMBL; BC022842; AAH22842.1; -.
HSSP; P08046; 1A1H.
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PRINTS; PR00048; ZINCFINGER.
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Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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Best Local Similarity
Matches 9; Conserv
                                                                                                                                                SEQUENCE FROM N.A.
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SEQUENCE
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Q92951;
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Qy 4 NTNKSEKAERKSHDTOTTQE 23
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                                                                                                                                                                                                                                                                                                                                                                707 NKSFKPNEKMHDKRSLQEVFE 727
                                                                                                                                                                                                                                                                                                                            6 NKSEKAERKSHDTQTTQEICE 26
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InterPro; IPRO00569; HECT_domain.
Pfam; PF00622; HECT; 1.
SMART; SM00119; HECTc; 1.
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                                                                                                                                                                                             Query Match 36.0%;
Best Local Similarity 47.6%;
Matches 10; Conservative
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Pfam; PF00037; fer4; 1
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Matches
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Nucleic Acids Res. 28:1397-1406(2000).
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STRAIN-NCTC 11168;
MEDIAM-20150912; PubMed=10688204;
Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C.,
Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S.,
Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W.,
Ouall M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
Whitehead S., Barrell B.G.;
"The genome sequence of the food-boine pathogen Campylobacter jejuni
reveals hypervariable sequences.";
Nature 403:665-668(2000).
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MEDLINE-20330349; PubMed-10871362;
Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K., Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Rukazawa T.;
Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
"Comparison of whole genome sequences of Chlamydia pneumoniae J138 from Japan and CWL029 from USA.";
Nucleic Acids Res. 28:2311-2314(2000).
EMBL; AE001617; AAD18480.1; -.
EMBL; AR002204; AAR58269.1; -.
EMBL; AP002546; BAA98541.1; -.
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Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
Campylobacter.
Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
                             Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
"Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
Nat. Genet. 21:385-389(1999).
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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InterPro; IPR001450; 4Fe4S_ferredoxin.
InterPro; IPR001413; AD-oxidase_C.
InterPro; IPR001575; Oxid_FAD_bind.
InterPro; IPR001467; Prok_Mboxred.
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                                                                                                                                                                                                                        MEDLINE=20150255; PubMed=10684935;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 30.89
Matches 8; Conservative
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                                                                                                                                                            SEQUENCE FROM N.A.
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   RAHRER KERKER KA
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                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                    Length 923;
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                                                                                                                                                              Score 50; DB 16; Length 92
Pred. No. 1.2e+02;
3; Mismatches 8; Indels
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                                    PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; UNKNOWN_1.
Complete proteome.
SEQUENCE 923 AA; 103909 MW; 06FC04D63259322A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases
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Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Utsugi T., Kikuchi Y.,
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U33050; AAB64910.1; -.
EMBL; D63905; BAA21482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
PROSITE; PS00198; 4FE4S_FERREDOXIN; 2.
PROSITE; PS00551; MOLYBDOPTERIN_PROK_1; UNKNOWN_1.
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Gaps

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RESULT 8

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Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S., Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T., Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A., Nakazaki N., Shimpo S., Sugimoto M., Takazawa M., Yamada M., Yasuda M., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Complete genomic sequence of the filamentous nitrogen-fixing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36.0%; Score 50; DB 16; Length 471; 45.5%; Pred. No. 60;
                                                                                                                                                                Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Anabaena sp. (strain PCC 7120).
Plasmid pCC7120beta.
Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
NCBI_TaxID=103690;
                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cyanobacterium Anabaena sp. strain PCC 7120.";
DNA Res. 8:205-213(2001).
ENEL, APO03602: BEB77290.1;
InterPro; IPR005094; Relaxase.
Pfam; PF03432; Relaxase; 1.
Plasmid; Hypothetical protein; Complete proteome.
Plasmid; Hypothetical protein; TDDBB895E220907E CRC64;
                                                                                                                            50793 MW; B38EAD4B4D0BEE6A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                      01-WAR-2002 (TrEMBLrel. 20, Created)
1-WAR-2002 (TrEMBLrel. 20, Last sequence update)
101-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein Alr7647.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CT082 hypothetical protein.
CPN0311 OR CPJ0331 OR CP0426.
Chlamydia pneumoniae (Chlamydophila pneumoniae).
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59;
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                                                                                                                                                              Score 50;
Pred. No. 5
                                                                                  TIGREAMS; TIGR01318; gltb_gamma_fam; 1. FAD; Flavoprotein; Oxidoreductase. SEQUENCE 465 AA; 50793 MW; B38EAD4B.
 InterPro; IPR000759; Adrndx_reductase.
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                   IPR001327; FAD_pyr_redox. IPR000205; NAD_binding.
                                                                                                                                                                                                                                                                                                                                                                     PRT;
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MEDLINE=21595285; Pubmed=11759840;
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MEDLINE-99206606; PubMed-10192388;
                                                                                                                                                                                                                                                              6 NKSEKAERKSHDTQTTQEIC 25
                                                                                                                                                                36.0%;
50.0%;
                                                   Pfam; PF00070; pyr_redox; 1 PRINTS; PR00419; ADXRDTASE.
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Best Local Similarity 45.5
Matches 10; Conservative
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10; Conserva
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                     InterPro;
                                      InterPro
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Best Local
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Q82S65;
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                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deane S.M., Rawlings D.E.; "The gene for the Thiobacillus ferrooxidans ATCC33020 glutamate synthase (GOGAT) small subunit complements an Escherichia coli gltD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
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NCBL_TaxID=920;
                                                                                                                                                                                                                                                                                                                                                                                                                     "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BRISTOL N2;
Scheet P., Gattung S.;
"The sequence of C. elegans cosmid B0261:";
Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases -!- COFACTOR: FAD (BY SIMILARITY). EMBL; U36427; AAA79783.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases EMBL; U97016; AAB52352.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 196 AA; 21516 MW; AFBFFBE84C60EF48 CRC64;
                                                                                                                            ul-JUL-1997 (TrEMBLrel. 04, Created)
01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Hypothetical 21.5 kDa protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Glutamate synthase small subunit gltD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      36.0%; Score 50; DB 5; ilarity 43.5%; Pred. No. 25; Conservative 5; Mismatches
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                     2 KPNTNK---SEKAERKSHDTQTTQEI 24
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                                                                                                                                                                                                                                                                                                                                                                  STRAIN=BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                        Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submission.";
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Best Local Similarity
Matches 10; Conserv
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11; Conservative
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Best Local Similarity
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            SEQUENCE FROM N.A.
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STRAIN=TLMV-NLC026;
MEDLINE=2048649; PubMed=10971131;
MEDLINE=2048649; PubMed=10971131;
Takabashi K., Hijikata M., Samckhvalov E.I., Mishiro S.;
Takabashi K., Hijilength nucleotide sequences of TT virus variants (types SANBAN and YONBAN) and the TT virus-like mini virus.";
Intervirology 43:119-123(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis."; Nat. Genet. 21:385-389(1999).
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                                                              Length 1048;
          SMART; SM00147; RasGEF; 1.
SMART; SM00229; RasGERN; 1.
PROSITE; PS00720; GDS_CDC25; 1.
SEQUENCE 1048 Aa; 121960 MW; 40AIF12F9B86F458 CRC64;
                                                                                                                                                                                                                                                                                                             Mishiro S., Hijikata M., Takahashi K.;
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria: Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAX-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SIMILARITY to CHLPS INCA (CPJ0585 protein).
CPN0585 OR CPJ0585 OR CP0163.
                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
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9
                                                             38.8%; Score 54; DB 3;
45.0%; Pred. No. 37;
tive 5; Mismatches 6
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                                                                                                                                                                                                                                                           ssDNA viruses; Circoviridae.
                                                                                                                                                                                                       Created)
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                                                                                                                     1002 PNSNSNNKSQEKSRDDQTDE 1021
                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB038630; BA8936091; '.'
InterPro: PR004219; TTVirus_Unk.
Pfam; PF02956; TT_ORT; 1.
SEQUENCE 661 AA; 78995 MW; 830
                                                                                                       3 PNTNKSEKAERKSHDTQTTQ 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Match 37.8%;
Local Similarity 51.7%;
les 15; Conservative 3
                                                                                                                                                                                                   01-0CT-2000 (TrEMBLrel. 15,
                                                                                                                                                                                                               01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21,
                                                  Pfam; PF00618; RasGEFN; 1.
                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                             TTV-like mini virus
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=TLMV-NLC026;
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                                                                                                                                                                                                                                                                  NCBI_TaxID=93678;
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                                                                                                                                                                                                                                                           Viruses;
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STRAIN=AR39;
MEDLINE-20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
Eisen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Schulsel J., Brandt P., Fartmann B., Holland R., Schultte U., Aign V., Hoheisel J., Brandt P., Fartmann B., Holland R., Nayakatura G., Mewes H.W., Mannhaupt G.; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                       "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae {\rm AR39.\,^{\prime\prime}};
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 642;
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Submitted (JAN-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AL356173, CAB91744.2;
InterPro; IPR002051; SAM.bind.
InterPro; IPR002792; TRAM.
InterPro; IPR001566; TrMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7EAC83171535CAB8 CRC64;
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Last annotation update)
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38.1%; Pred. No. 61;
ive 7; Mismatches 6,
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42.3%; Pred. No. 70;
tive 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          il protein; Complete proteome
651 AA; 75668 MW; 7EAC8317
                                                                                                                                                                                                                           Nucleic Acids Res. 28:1397-1406(2000).
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PROSITE; PS01231; TRMA_2; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                          MEDLINE=20330349; PubMed=10871362;
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TIGR; CP0163; -.
Hypothetical protein; Comple
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Matches 8; Conservative
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us-09-853-079-195.rspt

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Pfam; PF00617; RasGEF; 1.
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                                                           NCBI_TaxID=4932;
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                                                                                             MEDLINE-20231818; PubMed-10768973;
Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L.D.,
Benson D.R., Krause P.J., Reed S.G., Persing D.H.;
"Serological expression cloning of novel immunoreactive antigens of
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                               Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia
NCBI_TaxID=5868;
                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
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                                                                                                                                                                                               Length 396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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investigating biology.";
science 28:2012-2018(1998).
EMBL: Z69302: CAA93261.1;
Interpro; IPR003439; ABC_transportr.
PROSTIF; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
PROSTIF; PS00211; ABC_TRANSPORTER; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   MacDougall R.;
Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                           396 AA; 44720 MW; 706E153BA5EE6B7C CRC64;
                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Seroreactive antigen BMN1-17 (Fragment).
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(TrEMBLrel. 01, Last sequence update)
                                                                                                                                                                                             100.0%; Score 139; DB 5;
100.0%; Pred. No. 2.1e-11;
ive 0; Mismatches 0;
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Pred. No. 3.9;
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                                                                                                                                                                                                                                     1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                                                                                                                    Babesia microti.";
Infect. Immun. 68:2783-2790(2000).
EMBL; AF20623.1; -.
NON_TER 396 396
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52.2%;
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01-NOV-1996 (TrEMBLrel. 01,
01-DEC-2001 (TrEMBLrel. 19,
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Matches 12; Conservative
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Matches 26; Conserv
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                                       Babesia microti
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01-NOV-1996 (
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Miosga T., Zimmermann F.K.;
"Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 kb fragment of chromosome XII including an open reading frame homologous to the human cystic fibrosis transmembrane conductance regulator protein CFTR.";
Yeast 12:693-708(1996).
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MEDLINE=95348179; PubMed=7622557;
Gammie A.E., Kurihara L.J., Vallee R.B., Rose M.D.;
"DMM1, a dynamin-related gene, participates in endosomal trafficking in yeast.";
J. Cell Biol. 130:553-566(1995).
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STRAIN=FY23 / ROD055,
STRAIN=FY23 / ROD056,
MEDILINE=94375516; PubWed=8089172;
Burgess S.M., Delannoy M., Jensen R.E.;
Mundl encodes a mitochondrial outer membrane protein essential for establishing and maintaining the structure of yeast mitochondria.";
J. Cell Biol. 126:1375-1391(1994).
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STRAINE-Y23 / RD005;
MEDLINE-9087480; PubMed-1454790;
Ripmaster T.L., Vaughn G.P., Woolford J.L. Jr.;
Ripmaster T.L., vaughn G.P., Woolford J.L. Jr.;
"A putative ATP-dependent RNA helicase involved in Saccharomyces cerevisiae ribosome assembly.";
Proc. Natl. Acad. Sci. U.S.A. 89:11131-11135(1992).
                                                                                                                                                     Saccharomycetes;
                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-ALPHA S288C;
Purnelle B., Goffeau A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Sacch
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical protein L1309.
SDC25 OR SCD25 OR L1309/SCD25 OR YLL016W.
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EMBL, Z73121; CAA97461.1;

EMBL, X91488; CAA62775.1;

EMBL, X91488, CAA62775.1;

Interpro, IPR000651; RasGEFN.

Interpro, IPR001895; RasGRP_CDC25.
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STRAIN-FY23 /RD005;
MEDLINE-91094833; Pubmed=1986220;
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MEDLINE=96405918; PubMed=8810043;
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Submitted (MAY-1996) to t
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Q9fn33 arabidopsis
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09pmj6 campylobaci
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Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
NCBI_TaxID=5868;
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MEDLINE=20231818; PubMed=10768973;
Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L.D.,
Lodes D.R., Krause P.J., Reed S.G., Persing D.H.;
"Serological expression cloning of novel immunoreactive antigens of
Babesia microti.";
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275 275 W C3CC5D5EBC494E01 CRC64;
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01-077-2000 (TrEMBLrel. 15, Last sequence update)
01-077-2000 (TrEMBLrel. 15, Last annotation update)
Seroreactive antigen BMNI-20 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 139; DB 5;
100.0%; Pred. No. 1.4e-11;
Live 0; Mismatches 0;
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Q9R1Y9
Q9BJN1
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076734
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Q9VWQ6
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Q9Z2V0
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Q8W191
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Q9BZT7
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EMBL; AF206527; AAF68255.1; -.
Signal.
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SIGNAL
NON_TER
SEQUENCE
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Best Local
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Q9NIM4;
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ID O9
AC O9
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Q9nin4 babesia mic
Q2027 caenorhabdi
Q12037 saccharcomyc
Q91950 ttv-like mi
Q927w9 chlamydia p
Q8x093 neurospora
Q01439 caenorhabdi
Q55267 thiobacillu
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08sz45 drosophila
092951 homo sapien
09vby9 drosophila
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Q9z8k7 chlamydia p
Q9pm90 campylobact
                                                                                                                                                              (without alignments)
848.513 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                         July 16, 2003, 17:37:48; Search time 6.31366 Seconds
                   GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                       671580 segs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                090 NIM2
090 NIM4
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090 NIM6
090 NIM6
080 NIM6
090 NIM6
090
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_unclassified:*
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sp_phage:*
sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_bacteriap:*
sp_archeap:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 2000000000
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16
3
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16
16
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sp_virus:*
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Match Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                               Perfect score:
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60.5
54
52.5
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50.5
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                                                                                                                                                                                                                                                                     Sequence:
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                                                                                                                                             Run on:
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                                                                                                                                     ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hilbert H., Himmelreich R., Plagens H., Herrmann R.; "Sequence analysis of 56 kb from the genome of the bacterium Mycoplasma pneumoniae comprising the dnaA region, the atp operon and a cluster of ribosomal protein genes."

Nucleic Acids Res. 24:628-639(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 24:4420-4449(1996).
-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                Mycoplasma pneumoniae.
Bacteria: Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
NCBL_TaxID=2104;
                                                                                                                                     ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL LIPOPROTEIN MPN200.
N-ACYL DIGLYCERIDE (POTENTIAL).
3E2471D7EF0A3CAO CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE=97105885; PubMed-8948633;
Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45; DB 1; Length 798; Pred. No. 1e+02;
                                                                                                       Length 333;
                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical lipoprotein MPN200 precursor (GT9_orf798).
MPN200 OR MP631.
                                                            LYS-RICH.
88E91737402FC4CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE000060; AAB96279.1; -.
InterPro; IPR00489; Lipoprotein_10.
InterPro; IPR004984; Lipoprotein_X.
IPR03202; Lipoprotein_10; 1.
Pfam; PF03305; Lipoprotein_10; 1.
Hypothetical protein; Lipoprotein; Membrane; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (Potential).
-:- SIMILARITY: BELONGS TO THE MG185 / MG260 FAMILY.
                                                                                                     DB 1;
                                                                                                                                                                                                                                                                          798 AA
                                                                                                     Score 45; DB Dred. No. 43; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
           EMBL; 281035; CAB02731.1; -.
WormPep; C15H11.9; CE08186.
Ribosome biogenesis; Nuclear protein.
DOMAIN 79 332 LYS-RICH
                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-96177562; Pubmed-8604303;
                                                                                                                                                                3 PNTNKSEKAERKSHDTQTTQE 23
                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23 N
87628 MW;
                                                                        333 AA; 37985 MW;
                                                                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32.48;
                                                                                                     32.4%;
ilarity 47.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U34795; AAC43681.1; -.
                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22
798
                                                                                                     Query Match
Best Local Similarity
Matches 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             798 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Complete proteome
                                                                                                                                                                                                                                                                       YC00_MYCPN
Q50288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pneumoniae.
                                                          DOMAIN
SEQUENCE
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S FT S
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Best Local Similarity

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Gaps
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 8; Indels
 Mismatches
                                                                                      Search completed: July 16, 2003, 17:47:32
Job time : 3.53457 secs
                                          229 KKEEKKSTRSKRATEGTQTTKE 250
                          2 KPNTNKSEKAERKSHDTQTTQE 23
  2,
 9; Conservative
  Matches
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SGS3_DROYA
P13728:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          168
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                                                                                        SGS3_DROYA
                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 14
RRS1_CAEEL
  Matches
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          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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 the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -1 - MISCELLANEOUS: THIS PROTEIN HAS FOUR FUNCTIONAL CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toda H., Yazawa M., Yagi Y.;
"Amino acid sequence of calmodulin from Euglena gracilis.";
Eur. J. Blochem. 203:653-660(1992).
-!- FUNCTION: CALMODULIN MEDIATES THE CONTROL OF A LARGE NUMBER OF ENZYMES BY CA(++). AMONG THE ENZYMES TO BE STIMULATED BY THE CALMODULIN-CA(++) COMPLEX ARE A NUMBER OF PROTEIN KINASES AND PHOSPHATASES.
                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SIMILARITY: CONTAINS 4 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                            Length 533;
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                            POTENTIAL.
9492A18512F399CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Euglenozoa; Euglenida; Euglenales; Euglena.
NCBL_TaxID=3039;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       82A1E48108638455 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMARY; SW00054; EFP; 4.
PROSITE; PS00018; EF_HAND; 4.
Calcium-binding; Repeat; Acetylation; Methylation.
                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                    148 AA
                                                                                                                                                                                                                                  5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   METHYLATION.
METHYLATION.
EF-HAND 1.
EF-HAND 2.
EF-HAND 3.
                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACETYLATION
                                                                                                                      POTENTIAL. POTENTIAL.
                                                                                                                                                                                                             Score 46;
                                                                                                                                             POTENTIAL
                                                                                                                                                                   POTENTIAL
                                                                                                                                                        POTENTIAL
                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                           376 ESQDASTDRHDTSSNSEVCD 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN=Z;
MEDLINE=92241300; PubMed=1572365;
                                                                                                                                                                                                                                                        7 KSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIR; JK0008; MCEG.
PIR; S21212; S21212.
HSSP; P02593; ICDM.
InterPro; IPR002048; EF-hand.
Pfam; PP00036; efhand; 4.
ProDom; PD000012; EF-hand; 2.
                                                                                                                                                                                                                                                                                                                                                       01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last seq
30-MAY-2000 (Rel. 39, Last anno
                                                                                                                                                                                      MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16724 MW;
                                                                          EMBL; U23084; AAC49105.1; -. EMBL; Z11570; CAA56212.1; -. SGD; SGD05238; YNL294C. Hypothetical protein; Transme
                                                                                                                                                                                                            33.1%;
35.0%;
                                                                                                                                                                                                                      Best_Local Similarity 35.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                  115
148
199
                                                                                                                                           179 1
210 2
248 2
281 3
533 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                   Euglena gracilis.
                                                                                                                                                                                                                                                                                                                                                                   01-JUL-1989 (30-MAY-2000 (Calmodulin.
                                                                                                                                                                                                                                                                                                                                 CALM_EUGGR
P11118;
                                                                                                                                                                           TRANSMEM
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SITES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                       TRANSMEM
                                                                                                                                   TRANSMEM
                                                                                                                                            TRANSMEM
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                                                                                                                                                                   'RANSMEM
                                                                                                                                                                                                             Query Match
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MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CA_BIND
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                                                                                                                                                                                                                                                                                                                         CALM_EUGGR
                                                                                                                                                                                                                                                                                                             RESULT 12
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Length 148;

Score 45; DB 1; Pred. No. 19;

32.48; 64.38;

Best Local Similarity

Query Match

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 Gaps
                                                                                                                                                                                                                                                                                               Drosophila yakuba (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-88332966; PubMed-3138416;
Martin C.H., Mayeda C.A., Meyerowitz E.M.;
Martin and expression of the Sgs-3 glue gene of Drosophila.";
J. Mol. Biol. 201:273-287(1988).
-i- DEVELOPMENTAL STAGE: PRODUCED BY THIRD-INSTAR LARVAE.
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Pred. No. 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SALIVARY GLUE PROTEIN SGS-3.
C0C5246B482A261C CRC64;
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Ribosome biogenesis regulatory protein homolog
                                                                                                                                                                                                      01-JAN-1990 (Rel. 13, Created)
10-A02-1991 (Rel. 19, Last sequence update)
10-CCT-2001 (Rel. 40, Last annotation update)
Salivary glue protein Sgs-3 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  333 AA.
                                                                                                                                                                      263 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. 34;
6; Mismatches
 Mismatches
                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        :| || ::| :| :| HTTKSTTSKRPTHETTTTSK 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4 NTNKSEKAERKSHDTQTTQE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S01360; S01360.
FlyBase; FBgn0013172; Dyak\Sgs3.
1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-JUN-2002 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    263 S
28392 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32.4%;
40.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 40.000
Best Local Similarity 20.000
                                    13 RKSHDTQTTQEICE 26
9; Conservative
                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                       74 RKMHDTDTEEIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE 263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Repeat; Signal.
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                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Spectrin beta chain, brain I (Spectrin, non-erythroid beta chain 1)
(Beta-II spectrin) (Fodrin beta chain).
SPTBNI OR SPTB2 OR SPNB-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 14:4676-4681(1995).

-!- FUNCTION: FODRIN, WHICH SEEMS TO BE INVOLVED IN SECRETION,
INTERACTS WITH CALMODULIN IN A CALCIUM-DEPENDENT MANNER AND IS
THUS CANDIDATE FOR THE CALCUIM-DEPENDENT MOVEMENT OF THE
CYTOSKELETON AT THE MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Structure of the pleckstrin homology domain from beta-spectrin.";
                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE-92340985; PubMed-8479293;
MA Y., Zimmer W.E., Riederer B.M., Goodman S.R.;
"The complete amino acid sequence for brain beta spectrin (beta fodrin): relationship to globin sequences.";
Brain Res. Mol. Brain Res. 18:87-89(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Macias M.J., Musacchio A., Ponstingl H., Nilges M., Saraste M.,
Oschkinat H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'Structure of the binding site for inositol phosphates in a PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hyvoenen M., Macias M.J., Nilges M., Oschkinat H., Saraste M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -:- SIMILARITY: BELONGS TO THE SPECTRIN FAMILY.
-:- SIMILARITY: CONTAINS 2 CALPONIN-HOWOLOGY (CH) DOMAINS.
-:- SIMILARITY: CONTAINS 1 PH DOMAIN.
-:- SIMILARITY: CONTAINS 17 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 2199-2304. MEDLINE=96030773; PubMed=7588597;
                                                                            PRT; 2363 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:98388; Spnb2.
Inteerpro; IPR001589; Actbind_actnin.
Interpro; IPR001715; Calponin-like.
Interpro; IPR001849; PH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-94268558; PubMed-8208297;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97342712; PubMed-9199409;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    from beta-spectrin.";
J. Mol. Biol. 269:408-422(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRUCTURE BY NMR OF 2199-2304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 369:675-677(1994).
                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                              [1]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TETRAMERS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wilmanns M.;
                                                                          SPCO_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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STRAIN=S288c / FY1679;

MEDLINE=96132033; PubMed=8553702;

MEDLINE=96132033; PubMed=8553702;

MEDLINE=96132033; PubMed=8553702;

MEDLINE=96132033; PubMed=8553702;

"Sequence analysis of a 30 kb DNA segment from yeast chromosome XIV carrying a ribosomal protein gene cluster, the genes encoding a plasma membrane protein and a subunit of replication factor C, and a novel putative serine/threonine protein kinase gene.";

Yeast 11:1303-1310(1995).

-: SUBCELLULAR LOCATION: Integral membrane protein (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                         ### PF00169; PH; 1.
Pfam; PF00169; PH; 1.
Pfam; PF00307; CH; 2.
Pfam; PF00435; Spectrin; 18.
PRINTS; PR00603; SPECTRINPH.
SMART; SM00033; CH; 2.
SMART; SM00150; SPEC; 16.
PROSITE; PS00019; ACTININ_1; 1.
PROSITE; PS00020; ACTININ_2; 1.
PROSITE; PS50021; CH; 2.
PROSITE; PS50003; PH_LOMAIN; 1.

Cytoskeleton; Membrane; Repeat; Actin-binding; Capping protein;
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01-FEB-1996 (Rel. 33, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
Hypothetical 61.5 kDa protein in CLA4-PUS4 intergenic region.
                                                                                                                                                                                                       ACTIN-BINDING (BY SIMILARITY).
CH 1.
CH 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 47; DB 1; Length 2363; Pred. No. 1.7e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274420 MW; 64C9E4BD26BBC7B8 CRC64;
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SPECTRIN 2.
SPECTRIN 3.
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SPECTRIN 17
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                IPR001605; Spectrin_PH.
InterPro; IPR002017; Spectrin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.5%;
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1988 21:
2196 23:
2363 AA;
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                                                                                                                                                                                                                             3D-structure.
DOMAIN
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P48565;
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SEQUENCE
                  InterPro
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REPEAT
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VP6_AHSV6
Q64913:
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                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Baioinformatics and the FNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ibb-sib.ch).
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VPTRAPDAVYTELQPTSPTPTWPADETPQPQTQTQQLEGTD
GPLVTDPETHKSTKA -> MQTLSNIPCFCLHGSLLPSTDL
                                                                                  Omasa T., Chen Y.G., Mantalaris A., Wu J.H.D.;
"A cDNA from human bone marrow encoding a protein exhibiting homology
to the APPIL/PDM/MAR8 family of transmembrane proteins.";
Blochim. Blophys. Acta 1517:307-310(2001).
-: SUBCELLULAR LOCATION: Type I membrane protein (Potential).
-: SIMILARITY: BELONGS TO THE FXYD FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     African horse sickness virus 3 (AHSV-3) (African horse sickness virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                        FXXD DOMAIN-CONTAINING ION TRANSPORT REGULATOR 5.
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Pred. No. 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9; Indels
                             Submitted (JUN-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                  EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (IN DBSNP:1688005)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7429D5A838B75AA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                   Pfan, PF02038, ATPIG1_PLM_MAT8; 2.
PROSITE; PS01310; FXYD; 1.
Transmembrane; Signal; Ionic channel; Ion transport;
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Viruses; dsRNA viruses; Reoviridae; Orbivirus.
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VP6 protein (Minor inner core protein VP6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
                                                                                                                                                                                                                                                                                                           InterPro; IPR000272; ATP1G1_PLM_MAT8.
                                                                                                                                                                                                                                                                                                                                                    Alternative splicing; Polymorphism.
                                                               TISSUE-Bone marrow;
MEDLINE=21240216; PubMed=11342114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    89 PETHKSTKAAHPTDDTTTLSE 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PNTNKSEKAERKSHDTQTTQE 23
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                                                      SEQUENCE FROM N.A. (ISOFORM 2).
                                                                                                                                                                                                                                                    EMBL; AF161462; AAF29077.1; -. EMBL; BC009642; AAH09642.1; -. EMBL; AF177940; AAG09301.1; -.
SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 H
19453 MW;
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164
178
97
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178
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178 AA;
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                    Strausberg R.
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Q64909;
15-DEC-1998 (
15-DEC-1998 (
15-DEC-1998 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Turnbull P.J., Cormack S.B., Huismans H.; "Characterization of the gene encoding core protein VP6 of two African horsesickness virus serotypes.";
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Turnbull P.J., Cormack S.B., Hulsmans H.;
"Characterization of the gene encoding core protein VP6 of two
African horsesickness virus serotypes.";
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Pred. No. 25;
2; Mismatches 6; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    369 AA; 38464 MW; E696B1EF41A92768 CRC64;
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                                                                                          Gen. Virol. 77:1421-1423(1996).
SIMILARITY: BELONGS TO THE REOVIRUSES VP6 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J. Gen. Virol. 77:1421-1423(1996).
-!- SIMILARITY: BELONGS TO THE REOVIRUSES VP6 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
VP6 protein (Minor inner core protein VP6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (serotype 6)).
Viruses; dsRNA viruses; Reoviridae; Orbivirus.
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InterPro; IPR001399; Orbi_VP6.
Pfam; PF01516; Orbi_VP6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001399; Orbi_VP6.
Pfam; PF01516; Orbi_VP6; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6 NKSEKAERKSHDTQTTQ 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49 NKSEKEENKIHDDRRVE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 NKSEKAERKSHDTQTTQ 22
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NKSEKEENKIHDDRRVE 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.8%; 52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U19881; AAB17103.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 52.2.
Best Local 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=86060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-DEC-1998 (
15-DEC-1998 (
15-DEC-1998 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Core protein.
SEQUENCE 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Core protein
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MIM; 604502;
                                                                                                                                      receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its way non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
         Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

Theologis A., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Buehler E., Chan A., Chaof J., Chen H., Cheuk R.F., Chin C.W.,

Buehler E., Chan A., Chaof J., Chen H., Cheuk R.F., Chin C.W.,

Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

A. Dunn P., Etgu P., Feldhlyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A. Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,

A. Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,

A. Langin-Hooper S., Lee A., Lucos J.S., Maiti R., Marziali A.,

A. Milischer J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

Ran G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

W. D., Yu G., Fraser C.M., Veysbergia V.S., Walker M.,

"Sequence and analysis of chromosome I of the plant Arabidopsis
                                                                                                                                                                                                                                                                                          FUNCTION: CENTRAL COMPONENT OF THE RECEPTOR COMPLEX RESPONSIBLE FOR THE RECGRITION AND TRANSLOCATION OF CYTOSOLICALLY SYNTHESIZED MITOCHONDRIAL PREPROPEINS. TOGETHER WITH TOWLZ FUNCTIONS AS THE TRANSIT PEPTIDE RECEPTOR AT THE SURREACE OF THE MITOCHONDRION OUTER MEMBRANE AND FACILITATES THE MOVEMBNT OF PREPROTEINS INTO
                                                                                                                                                                                                                                                                                                                                                                                                                           PTM: THE N-TERMINUS IS BLOCKED.
MISCELLANEOUS: THERE ARE FOUR GENES (TOM20-1, TOM20-2, TOM20-3 AND TOM20-4) WHICH ENCODE MITOCHONDRIAL IMPORT RECEPTOR SUBUNITS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: FORMS PART OF MITOCHONDRIAL RECEPTOR COMPLEX. SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Transport; Protein transport; Outer membrane; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.3%; Score 49; DB 1; Length 210; 28.0%; Pred. No. 7.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Thyroid receptor interacting protein 7 (TRIP7) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERMEMBRANE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F -> L (IN REF. 2).
MISSING (IN REF. 2).
65EA3327249A62E2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE TOM20 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 160 GMASSNVSQSSKKKKRNTEFTYDVC 184
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MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AJ296024; CAC14429.1; -. EMBL; AC004557; AAF99745.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23204 MW;
                                                                                                                                                                                                                                                                                                                                                                     THE TRANSLOCATION PORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7; Conservative
                                                                                                                                                                                                                                                                             Nature 408:816-820(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                  outer membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       210 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
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11
168
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Q15651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                     MOI. Endocrinol. 9:243-254(1995).

-!- FUNCTION: INTERACTS, IN VITRO, WITH THE LIGAND BINDING DOMAIN OF THE THYROID RECEPTOR (TR). TRIP7 REQUIRES THE PRESENCE OF THYROID HORMONE FOR ITS INTERACTION.

-!- SUBCELLULAR LOCATION: Nuclear.

-!- SUBCELLULAR LOCATION: Nuclear.

-!- TISSUE SPECIFICITY: ABUNDANTLY EXPRESSED IN KIDNEY, SKELETAL MUSCLE AND HEART. LOWER LEVELS FOUND IN LUNG, LIVER AND PANCREAS.

-!- SIMILARITY: BELONGS TO THE HMG-14/HMG-17 PROTEIN FAMILY.
                                                                                                                                                                                                                       Lee J.W., Choi H.-S., Gyuris J., Brent R., Moore D.D.; "Two classes of proteins dependent on either the presence or absence of thyroid hormone for interaction with the thyroid hormone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .;
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(Dysadherin) (HSPC113).
FXYD5 OR IWU1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     33.8%; Score 47; DB 1; Length 120; 37.5%; Pred. No. 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 120 AA; 13016 MW; 2B7A0B9D352BF78F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FXY5_HUMAN STANDARD; PRT; 178 AA. Q96DB9; Q9PQ34; 09HC34; 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update) 15-JUN-2002 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000079; Highmoblty_14_17.

Pfam; PF01101; HMG14_17; 1.

SMART; SM00527; HMG14_17; 1.

PROSITE: PS00355; HMG14_17; 1.

Nuclear protein; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GKPNTNKSEKAERKSHDTQTTQEI 24
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MEDLINE-20499367; PubMed-11042152;
                                                                                                                                                                                        MEDLINE=95295737; PubMed=7776974;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 1).
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Genome Res. 10:1546-1560(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; L40357; AAA73877.1; -. Genew; HGNC:12312; TRIP7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 37.55
Local 9, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
                                                                                                                                             SEQUENCE FROM N.A.
                                                                              NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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SEQUENCE FROM N.A. STRAIN=cv. Columbia;
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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OM22_ARATH
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    δλ
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                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Burpaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
0
                                    Oncogene 6:347-349(1991).
-!- FUNCTION: PROMOTES THE EXCHANGE OF RAS-BOUND GDP BY GTP.
-!- MISCELLANEOUS: SUPPRESSES THE CDC25-5 MUTATION IN YEAST (RESTORES CAMP LEVEL) NND HAS SIMILAR FUNCTIONS AS CDC25.
-!- SIMILARITY: CONTAINS 1 SH3 DOMAIN.
-!- SIMILARITY: CONTAINS 1 RAS-GEF DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
"The COOH-domain of the product of the Saccharomyces cerevisiae gene elicits activation of p21-ras proteins in mammalian cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Guanine-nucleotide releasing factor; Cell cycle; Cell division;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
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MEDLINE=9728161; PubMed-9136770;
Habsaki K., Staunton J., Saifee O., Nonet M., Thomas J.H.;
"aex-3 encodes a novel regulator of presynaptic activity in C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10 DVVVKFI -> V (IN STRAIN 0L136).
144979 MW; 2DE2C9EC27E3E60D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 54; DB 1; Length 1253;
Pred. No. 9.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AEX3_CAEEL STANDARD; PRT; 1409 AA. 002626; 027467; 16-072001 (Rel. 40, Last sequence update) 16-077-2001 (Rel. 40, Last sequence update) 16-077-2001 (Rel. 40, Last annotation update) Regulator of presynaptic activity aex-3. Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rhabditidae; Peloderinae; Caenorhabditis.
NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            POLY-ASN.
POLY-ARG.
                                                                                                                                                                                                                                                                                                                                                                   PIR: S14177; S14177.
SGD: S0003939; SDC25.
InterPro: IPR000651; RasGEFN.
InterPro: IPR001895; RasGRF_CDC25.
InterPro: IPR001495; SH3.
Ffam: PF00618; SH3.
Pfam: PF00618; RasGEFN: 1.
Pfam: PF00618; RasGEFN: 1.
SWART: SW00147; RasGEFN: 1.
SWART: SW00229; RASGEFN: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ||:|: |: || ||:
1207 PNSNSNNKSQEKSRDDQTDE 1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3 PNTNKSEKAERKSHDTQTTQ 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00720; GDS_CDC25; 1. PROSITE; PS50002; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                    EMBL; M26647; AAA16565.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        38.8%;
45.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuron 18:613-622(1997).
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79
437
590
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74 7
434 43
584 59
1253 AA;
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SEQUENCE
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation: the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                               in synaptic transmission.";
EMBO J. 13:4806-4816(2000).
-!- FUNCTION: GUANINE NUCLEOTIDE EXCHANGE FACTOR (GEF) FOR RAB3. MAY
REGULATE TWO DIFFERENT PATHWAYS FOR NEURAL ACTIVITIES.
                                                          INTERACTION WITH CAB-1.
MEDLINE=20428446; PubMed=10970871;
Iwasaki K., Toyonaga R.;
The rab3 GDP/GTP exchange factor homolog AEX-3 has a dual function
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM22_ARATH STANDARD; PRT; 210 AA.
P02873; OSFZJ6;
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Mitochondrial import receptor subunit TOM20-2 (Translocase of outer membrane 20 kpa subunit 2).
TOM20-2 OR ATIG27390 OR F17L21.18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Purification and characterization of the preprotein translocase of the outer mitochondrial membrane from Arabidopsis thaliana. Identification of multiple forms of TOM20."; Plant Physiol. 125:943-954(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 50; DB 1; Length 1409;
Pred. No. 39;
                                                                                                                                                                                                                                                                                                                           -i- SUBUNIT: BINDS TO CAB-1.
-i- TISSUE SPECIFICITY: EXPRESSED IN A VARIETY OF NEURONS.
-i- SIMILARITY: CONTAINS 1 DENN DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32 SER-RICH.
157458 MW; 2DDE6395AC963313 CRC64;
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Submitted (FEB-1996) to the EMBL/GenBank/DDBJ databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U93842; AAB52421.1; -.
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PubMed=11161051;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crechet J.B., Poullet P., Mistou M.-Y., Parmeggiani A., Camonis J., Boy-Marcotte E., Damak F., Jacquet M.; "Enhancement of the GDP-GTP exchange of RAS proteins by the carboxyl-terminal domain of SCD25."; Science 248:866-868(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Damak F., Boy-Marcotte E., le Roscouet D., Guilbaud R., Jacquet M.;
"SDC25, a CDC25-like gene which contains a RAS-activating domain and is a dispensable gene of Saccharomyces cerevisiae.";
Mol. Cell. Biol. 11:202-212(1991).
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Gullbaud R., Jacquet M., Tocque B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 1158;
                                                                                                                                                                                                                                                                                                                                                             Transcription regulation, Nuclear protein.

CONFLICT 124 124 P -> R (IN REF. 1).

CONFLICT 448 448 R -> G (IN REF. 1).

CONFLICT 721 726 NKGKSE -> TKGRVK (IN REF. 1).

CONFLICT 1080 1080 T -> A (IN REF. 1).

SEQUENCE 1158 AA; 126941 MW; 81FC424968E9A5F6 CRC64;
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15-JUN-2002 (Rel. 41, Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                         EMBL; AF248484; AAF62185.1; -. EMBL; AF127577; AAF35255.1; -. EMBL; AL163207; CAB90396.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.8%;
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SCD25 OR SDC25 OR YLL016W.
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                                                                                                                                                                                                                                                                                                                   Genew; HGNC:8001; NRIPl.
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12; Conserv
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P14771;
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Best Local :
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Hattori M., Fujlyama A., Taylor T.D., Watanabe H., Yada T.,
Hattori M., Fujlyama A., Taylor T.D., Watanabe H., Yada T.,
Hattori M., Fujlyama A., Taylor T.D., Watanabe H., Yada T.,
Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
Menzel U., Delabar J., Schillhabel M., Schudy A., Zihmermann W.,
Rosenthal A., Kump A., Schillhabel M., Schudy A., Zihmermann W.,
Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E.,
Minoshima S., Shiniau N., Nordaske G., Hornischer K., Brandt P.,
Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloceker H.,
Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E.,
Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- FUNCTION: MODULATES TRANSCRIPTIONAL ACTIVATION BY THE ESTROGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                  Prim: PF00226; Dnad; 1.
Pfam; PF00684; Dnad_CXXCXGXG; 1.
Pfam; PF01686; Dnad_C; 1.
PRINTS; PF01685; DNAJ_PROTEIN.
SMART; SM00271; DnaJ; 1.
SMOSITE; PS00635; DNAJ_1; 1.
PROSITE; PS00637; DNAJ_2; 1.
PROSITE; PS00705; DNAJ_2; 1.
Chaperone; Heat shock; Mitochondrion; Repeat; Transit peptide.
TRANSIT 1 55 MITOCHONDRION (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 511;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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Last annotation update)
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"The DNA sequence of human chromosome 21.";
Nature 405:311-319(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                  CXXCXGXG MOTIF
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Pred. No. 2.1;
2; Mismatches
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GLY-RICH.
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       DnaJ_CXXCXGXG
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MEDLINE=95369246; PubMed=7641693;
IPR001305; DnaJ_CXXC;
IPR001623; DnaJ_N.
IPR003095; HSp_DnaJ.
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16-OCT-2001 (Rel. 40, Last sequ
15-JUN-2002 (Rel. 41, Last anno
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50.0%;
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186
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16-OCT-2001
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P48552;
                                                      InterPro;
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DOMAIN
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                                                                                                                                                    July 16, 2003, 17:37:24; Search time 1.53457 Seconds (without alignments) 702.729 Million cell updates/sec
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P1852
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                        US-09-853-079-195
139
1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                            112892 seqs, 41476328 residues
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YCOO_MYCPN
YMSI_YEAST
RBMA_HUMAN
NFH_HUMAN
CENC_MOUSE
RL32_DEIRA
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SC25_YEAST
AEX3_CAEEL
AEX3_CAEEL
TRI7_HUMAN
FXY5_HUMAN
VP6_AHSV6
SPCO_MOUSE
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CALM_EUGGR
SGS3_DROYA
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Maximum Match 100%
Listing first 45 summaries
                                                                                                   - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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seq length: 200000000
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Match
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RESULT 1 RESULT 1 AC P3513 AC P3513 DD T O1-FEAT DD T O1-FEAT AD D1 ND T O1-FEAT AD D1 ND T O1-FEAT AD D1 ND T O1-FEAT BEAT OF CO EACAN RESULT 1 AC O1-FEAT AC O1-FEAT BEAT O1-FEAT BEAT O1-FEAT BEAT O1-FEAT RESULT 1 AC O1-FEAT AC O1-FEAT BEAT O1-FEAT	43 30.9 440 1 FUIO_ARATH Q95jp6 arabidopsis 43 30.9 547 1 OM6C_CHLTR P26758 chlamydia t 43 30.9 547 1 OM6C_CHLTR P28563 chlamydia t 43 30.9 547 1 OM6C_CHLTR P23563 chlamydia t 43 30.9 547 1 OM6C_CHLTR P21354 chlamydia t 43 30.9 577 1 MTG8_MOUSE Q61909 mus musculu 43 30.9 674 1 MTG8_MOUSE Q61909 mus musculu 43 30.9 703 1 MTSB_MTJA Q61812 methañococc 43 30.9 703 1 MTSL_HUMAN Q15234 homo sapien Q9wv04 mus musculu 43 30.9 790 1 KIF9_MOUSE Q9wv04 mus musculu 43 30.9 862 1 RBMA_RAT Q00132 ictalurid h	ALIGNMENTS	YEAST STANDARD; PRT; 511 AA B-1994 (Rel. 28, Created) B-1994 (Rel. 28, Last sequence update)	(rel. 41, , mitocho 16C. s cerevis ungi; Asc tales; Sa	[1] SEQUENCE FROM N.A. SYRAIN=S288C / AB972; SWATAN=S288C / AB972; Rowley N.K., Prip-Buus C., Westermann B., Brown C.M., Schwarz E., Barrell B.G., Neupert W.; Submitted (NoV-1993) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. SERAIN-S288c / AB972; Barrell B.G., Churcher C., Rajandream M.A.; Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.	SEQUENCE FROM N.A. STRAIN=S288C / AB972; MEDLINE=59400292; PubMed=7670463; Murakami Y., Naitou M., Hagiwara H., Shibata T., Ozawa M., Sasanuma SI., Sasanuma M., Tsuchiya Y., Soeda E., Yokoyama K.,	arysis of the increoling sequence of chromosome vi iron charomyces cerevisiae."; Genet. 10:261-268(1995). FUNCTION: PLAYS A ROLE IN MITOCHONDRIAL BIOGENESIS AND PROTEIN FOLDING. SUBCELLULAR LOCATION: Mitochondrial. SIMILARITY: CONTAINS 1 J DOMAIN. SIMILARITY: CONTAINS 1 CR DOMAIN.	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).	EMBL; 228336; CAA82189.1; EMBL; 246255; CAA86331.1; EMBL; D50617; BAA09222.1; PIR; S38898; S38989. PIR; S48320; S48320. HSSP; P08622; BQ2. SGD; S0001878; MDJ1. InterPro; IPR002939; DnaJ_C.
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			MAR		RP RC RA RA	RP RC RA	RA R R R R R R R R R R R R R R R R R R	7 E 7 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	88888888	D D D D D D D D D D D D D D D D D D D
										

archaeoglob cyanidium c mycoplasma

HUNB_MANSE VP6_BTV1S SLAM_MOUSE PESC_SCHPO YJL3_YEAST YK01_ARCFU RK32_CYACA RR32_XYCPN RL32_XYLFA

44 44 43.5 43

xylella fas photobacter schizosacch

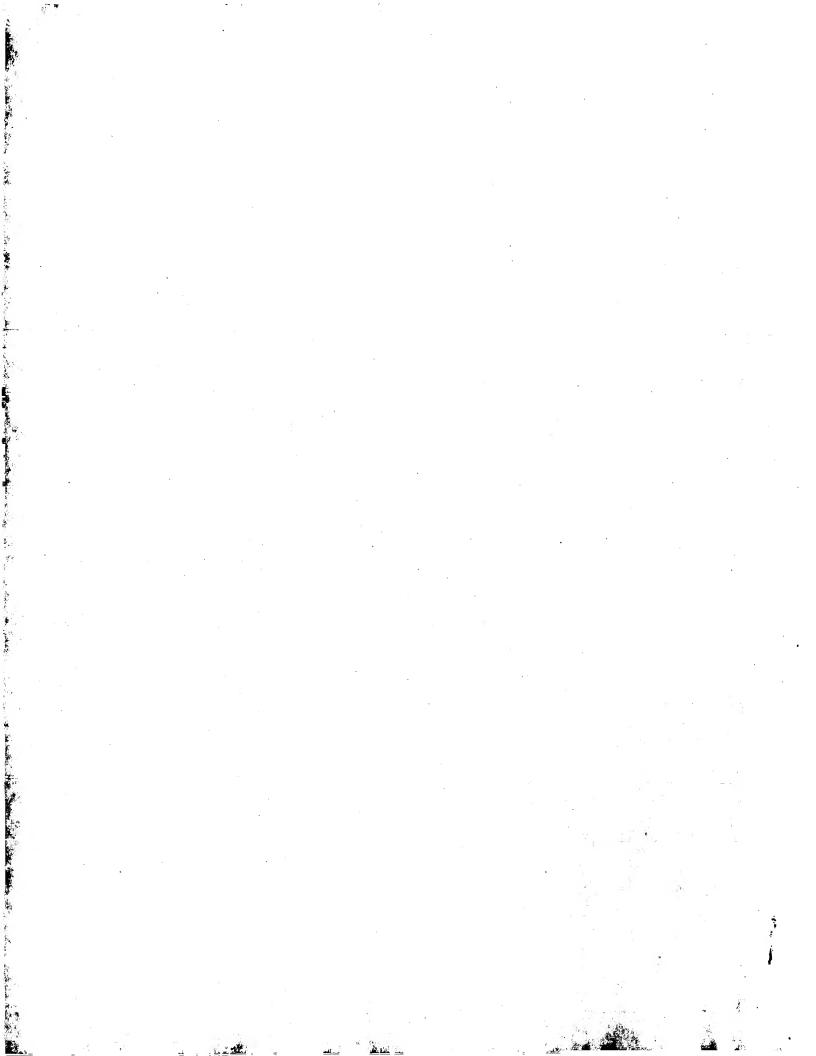
mus musculu deinococcus manduca sex mus musculu schizosacch saccharomyc

bluetongue

homo sapien chlamydia m

P87126 Q9unh7 Q9pjg1

SNX6_HUMAN Y868_CHLMU CWF2_SCHPO



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Submitted to the EMBL Data Library, August 1995
A;Description: The sequence of S. cerevisiae cosmids 9410, 8035, 8166, and 9787.
A;Reference number: 869554
A;Accession: 869625
A;Accession: 869625
A;Accession: A;Ac
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C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
C;Accession: T40036
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Lauber, J.; Hilbert, H.; Duesterhoeft, A.submitted to the EMBL Data Library, December 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-803 <WOO>
A;Cross-references: EMBL:AL021766; PIDN:CAA16907.1; GSPDB:GN00067; SPDB:SPBC27B12.12c
A;Experimental source: strain 972h-; cosmid c27B12
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hypothetical protein YDR457w - yeast (Saccharomyces cerevisiae)
C;Species: Saccharomyces cerevisiae
C;Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 23-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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56;
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Pred. No. 56;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: SGD:TOM1
A;Cross-references: SGD:S0002865; MIPS:YDR457w
A;Map position: 4R
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34.8%;
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Best Local Similarity 44.0%;
Matches 11; Conservative
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Best Local Similarity 34.8%
Matches 8; Conservative
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A;Gene: SPDB:SPBC27B12.12c
A;Map position: 2
                                                                                                                                                   Accession: $69625
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Gaps

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Indels

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Cyaccession: G81233
Ryparkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chill
C.W.; Ouail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, S.; Bar
Nature 403, 665-668, 2000
A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals
A;Reference number: A81250; MUID:20150912; PMID:10688204
A;Accession: G81253
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-923 cPAR>
A;Residues: 1-923 cPAR>
A;Experimental source: serotype 02, strain NCTC 11168
A;Experimental source: serotype 02, strain NCTC 11168
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                                                                                                                                                                                                                                                                                                                                   probable oxidoreductase Cil585c [imported] - Campylobacter jejuni (strain NCTC 11168)
C;Species: Campylobacter jejuni
C;Date: 31-Mar_2000 #sequence_revision 31-Mar-2000 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               presynaptic activity regulator aex-3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 18-Feb-2000
C;Accession: T37188
R;Leimbac, D.; Minx, M.
submitted to the EMBL Data Library, February 1996
A;Description: The sequence of C. elegans cosmid C02H7.
A;Reference number: Z20523
A;Accession: T37188
A;Status: translated from GB/EMBL/DDBJ
A;Residues: translated from GB/EMBL/DDBJ
A;Residues: 1-1409 <LEET>
A;Cross-references: EMBL: U49945; PIDN:AAC47926.1; GSPDB:GN00029
A;Experimental source: strain Bristol N2; clone C02H7
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                                                               ; Score 50; DB 2; Length 579;
; Pred. No. 29;
10; Mismatches 8; Indels
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Pred. No. 46;
3; Mismatches
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                                                                                                                                                                   1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                                                       36.0%;
30.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 36.0%;
Best Local Similarity 47.6%;
Matches 10; Conservative
                                             Query Match
Best Local Similarity 30.00
The By Conservative
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Matches 8; Conserv
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C;Genetics:
A;Gene: CPj0331
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S69625
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A;Cross-references: GB:AE002204; GB:AE002161; NID:g7189350; PIDN:AAF38269.1; PID:g718935
A;Experimental source: strain AR39, HL cells
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A:Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
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               A: Residues: 1-471 CKUR>
A:Cross-references: GB:AP003602; PIDN:BAB77290.1; PID:g17134732; GSPDB:GN00181
A:Experimental source: strain PCC 7120
C:Genetics: A:Genetics: A:Genewe: plasmid
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A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-579 <STO>
A; Cross-references: GB:BA000008; NID:g8978705; PIDN:BAA98541.1; GSPDB:GN00142
A; Experimental source: strain J138
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29;
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                                                                                                                                                                                          Score 50; DB;
Pred. No. 24;
4; Mismatches
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Matches 8; Conserv
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Best Local Similarity
Matches 10; Conserv
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A; Molecule type: DNA
A; Residues: 1-579 <ARN>
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A; Molecule type: DNA
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Length 923; 8; Indels ö

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G; Species: Thiobacillus ferrooxidans C; Species: Thiobacillus ferrooxidans C; Species: Thiobacillus ferrooxidans C; Date: 16 Feb-1997 #sequence_revision 27 Feb-1997 #text_change 29-Sep-1999 C; Accession: JC5184 G; A; Rawlings, D. E. R. Deane, S. M.; Rawlings, D. E. A; Title: Cloning and sequencing of the gene for the Thiobacillus ferrooxidans ATCC330 A; Reference number: JC5184; MUID:97080532; PMID:8921877 A; Status: preliminary; nucleic acid sequence not shown A; Status: preliminary; nucleic acid sequence not shown A; Residues: 1-465 < DEA>
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A,Note: Nostoc sp. Strain pcc 7120 is a synonym of Anabaena sp. strain pcc 7120
C,Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 30-Jun-2002
C,Accession: AD2545
R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Status: preliminary
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F:151-156,291-296/Region: glycine-rich
F:47-437/Region: FAD-binding #status predicted
F:45,48,53,57,92,96,102,106/Binding site: Iron-sulfur clusters (Cys) (covalent) #stat
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                                                                                                                                                                                                                                                         A; Residues: 1-196 <SCH>
A; Cross-references: EMBL:U97016; PIDN:AAB52352.1; GSPDB:GN00019; CESP:B0261.5
A; Experimental source: strain Bristol N2; clone B0261
C; Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
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A;Experimental source: strain ATCC33020
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                                                                                   Library, April 1997
s of C. elegans cosmid B0261
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A;Molecule type: DNA
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2; Mismatches
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Pred. No.
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Matches 10; Conservative
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                                                     R;Scheet, P.; Gattung, S. submitted to the EMBL Data
                                                                                                                                              A; Reference number: Z20036
A; Accession: T25445
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Best Local Simi
Matches 10;
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A;Introns: 162/3
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C; Accession: R6563
R; Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
Nucleic Acids Res. 28, 2311-2314, 2000
A; Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A; Reference number: A86491; MUID:20330349; PMID:10871362
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A; Residues: 1-651 CARNA
A; Cross-references: GB: AE001643; GB: AE001363; NID: 94376876; PIDN: AAD18724.1; PID: 9437687
A; Experimental source: strain CWL029
B; Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Godson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucle: Acids Res. 28, 1397-1406, 2000
A; Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
A; Reference number: A81500; MUID: 20150255; PMID: 10684935
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A;Experimental source: strain AR39, HL cells
C;Genetics:
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A;Title: Comparative genomes of Clamydia pneumoniae and C. trachomatis.
A;Reference number: A72000; MUID:99206606; PMID:10192388
                                                                                                             hypothetical protein CPj0585 [imported] - Chlamydophila pneumoniae (strain J138) C.Species: Chlamydophila pneumoniae, Chlamydia pneumoniae (C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 02-Mar-2001 C.Accession: F86563
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24;
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Pred. No.
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Pred. No.
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38.1%;
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Best Local Similarity
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A;Molecule type: DNA
A;Residues: 1-651 <REA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Gene: CPj0585
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A; Molecule type: DNA
A; Residues: 1-1048 <MIW>
A; Residues: 1-1048 <MIW>
A; Cross-references: EMBL:X91488; NID:g1495203; PIDN:CAA62775.1; PID:g1495207
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, September 199
C; Genetics:
                                                                                   A;Title: Sequence analysis of the CEN12 region of Saccharomyces cerevisiae on a 43.7 e conductance regulator protein CFTR.
                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Map position: 12L C;Superfamily: CDC25-type guanine nucleotide exchange activator homology F;744-995/Domain: CDC25-type guanine nucleotide exchange activator homology
  A:Cross-references: EMBL:X97560; NID:g1297003; PID:e238680; PID:g1297014 R:Miosga, T.; Zimmermann, F.K.
Yeast 12, 693-708, 1996
                                                                                                                                               A; Reference number: $70557; MUID:96405918; PMID:8810043
A; Accession: $70559
A; Status: nucleic acid sequence not shown; translation not shown A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 54; DB 2
Pred. No. 14;
5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                            A; Cross-references: SGD:S0003939; MIPS:YLL016w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1002 PNSNSNNKSQEKSRDDQTDE 1021
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45.0%;
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Similarity 45.0%;
9; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                 A; Gene: SGD:SCD25; SDC25
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Superfamily: heat shock protein dnaJ; dnaJ amino-terminal homology

Keywords: heat shock; membrane protein; mitochondrial inner membrane; mitochondrion; m
1-55/Domain: transit peptide (mitochondrion) #status predicted <TNP>
56-511/Product: heat shock protein MDJ1 #status predicted <MAT>
61-125/Domain: dnaJ amino-terminal homology <DNJ>
Cell 77, 249-259, 1994

Yittle: Mdjlp, a novel chaperone of the DnaJ family, is involved in mitochondrial bioge A; Reference number: A53500; MUID:94221642; PMID:8168133
A; Accession: A55500
                                                                                                                                                                    A;Cross-references: GB:Z28336; NID:g431909; PIDN:CAA82189.1; PID:g431910
R;Murakami, Y.; Naitou, M.; Hagiwara, H.; Shibata, T.; Ozawa, M.; Sasanuma, S.I.; Sasanu Submitted to the EMBL Data Library, May 1995
A;Description: Analysis of the nucleotide sequence of chromosome VI from Saccaromyces ce A;Reference number: S56186
                                                                                                                                                                                                                                                                                                                            14
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A;Residues: 1-1048 <MIO>
A;Cross-references: EMBL:Z73121; NID:91360186; PID:e245452; PID:91360187; MIPS:YLL016w
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A; Description: The sequence of 32 kb on the left arm of yeast chromosome XII reveals mily and a new ABC transporter homologous to the human multidrug resistance protein. A; Reference number: $69380
A; Recession: $69390
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A;Residues: 1-511 <MUW>
A;Cross-references: EMBL:D44596; NID:g1100783; PIDN:BAA08001.1; PID:g1100788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N.Alternate names: protein Li309; protein Li309. Catevisiae)
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisiae
C;Saccession: S64758; S64764; S69390; S70559
R;Miosga, T.; Zimmermann, F.K.
submitted to the Protein Sequence Database, May 1996
A;Reference number: S64743
A;Reference number: S647758
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R; Goffeau, A.; Purnelle, B.
submitted to the Protein Sequence Database, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, December 1994 A; Reference number: $62230 A; Accession: $62297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 56;
Pred. No.
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A;Cross-references: EMBL:273121; NII
A;Experimental source: strain S288C
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1 Similarity 50.0%;
11; Conservative 5
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A; Accession: $64764
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                                                                                                                 A; Molecule type: DNA
A; Residues: 1-511 <RO2>
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A;Title: The C-terminal part of a gene partially homologous to CDC25 gene suppresses A;Reference number: PSO041; MUID:89306677; PMID:2245538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Superfamily: CDC25-type guanine nucleotide exchange activator homology F;946-1197/Domain: CDC25-type guanine nucleotide exchange activator homology <SOS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                                                                                                  A; Wolecule type: DNA
A; Residues: 1-1250 < CDAM1>
A; Cross-references: EMBL:M26647
A; Cross-references: EMBL:M26647
B; Damak, F.; Boy-Marcotte, E.; Le-Roscouet, D.; Guilbaud, R.; Jacquet, M.
Mol. Cell. Biol. 11, 202-212, 1991
A; Title: SDC25, a CDC25-11ke gene, which contains a RAS-activating domain and
A; Reference number: $12942; MUID:91094833; PMID:1986220
SCD25 protein (version 1) - yeast (Saccharomyces cerevisiae)
N;Alternate names: protein L1309; protein YLL016w
C;Species: Saccharomyces cerevisiae
C;Species: Saccharomyces cerevisian
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 06-Feb-1998
C;Accession: S14177; S12942; PS0040
R;Damak, F.; BOY-Marcotte, E.; Le-Roscouet, D.; Guilbaud, R.; Jacquet, M. A;Reference number: S14177
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residue 747
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Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-737,'A',738-970,'I',972-1250 <DAM2>
A;Cross-references: EMBL:M26647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 668-679, 'NPVMTILMC', 689,'N', 691-1250
A; Note: the authors translated the codon GCA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5; Mismatches
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A;Map position: 12L
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Gaps

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Length 1048;

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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 16, 2003, 17:50:14 ; Search time 3.06914 Seconds (without alignments) 814.396 Million cell updates/sec Run on:

US-09-853-079-195 Perfect score: Title:

139 1 GKPNTNKSEKAERKSHDTQTTQEICE 26 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283224 seqs, 96134422 residues Searched:

283224 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

PIR_73:* Database :

pirl:* pir2:* pir3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	hypothetical prote	rotei	prote		a	hypothetical prote		qlutamate synthase	hypothetical prote	conserved hypothet	CI082 hypothetical	probable oxidoredu	presynaptic activi	hypothetical prote	hypothetical prote	GTP pyrophosphokin	probable hemolysin	probable RNA helic	hypothetical prote					Н	hypothetical prote		Ω	probable membrane	hypothetical prote
SUMMARIES	OI.	T22033	838888	S64758	S14177	F86563	A72060	T25445	JC5184	AD2545	D72092	C86532	G81253	T37188	S69625	T40036	E69844	F71374	A86444	F71621	T09076	T45622	G81292	F96831	T10457	T28053	T23785	н90266	S63270	.T25572
	Length DB	879 2			1250 2																				7	225 2	e	e	m	608 2
о¥	Query Match I	43.5	40.3	38.8	38.8	36.7	36.7	36.0	36.0	36.0	36.0	36.0	36.0	36.0	36.0	35.3	34.2	33.8	33.8	33.8	33.8	33.8	33.5	33.5	33.1	33.1	33.1	33.1	33.1	33.1
	Score	60.5	26	54	54	51	. 51	20	20	20	20	20	20	20	20	49	47.5	47	47	47	47		46.5	9	46	46	46	46	46	46
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B69797 C95046	T49758 T13115 T33810	T34243 T19899	MCEG S01360	T47695 T19313	T46464 T02022	A45294 S66719	S62791
22	0 0 0	0.0	7	7 7	7 7	7 7	7
761	831 631 881	890 1230	148 263	$\frac{310}{333}$	542 543	749	798
33.1	33.1 32.7 32.7	32.7	32.4 32.4	32.4	32.4 32.4	32.4	32.4
4 4 6 6 6	45.5 45.5 45.5	45.5	45 45	45 45	4 5	4 4 5	45
30	3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	35 36	37 38	39 40	41 42	43 44	45

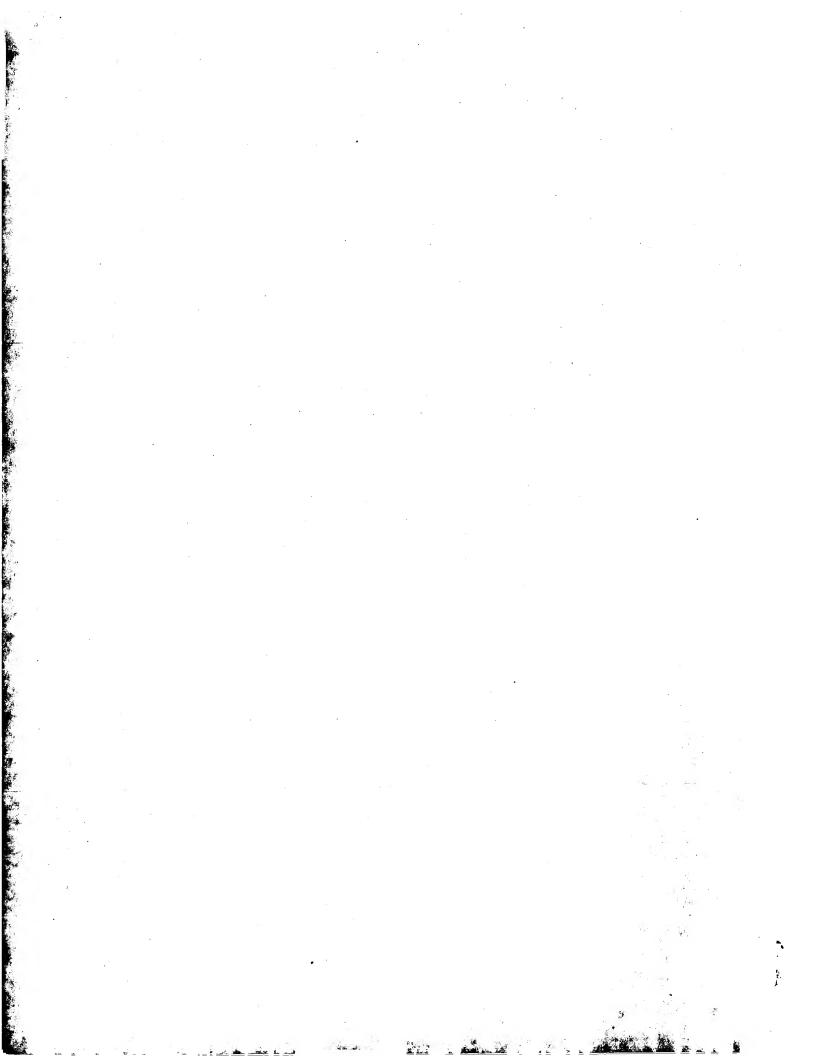
ALIGNMENTS

15-0ct-1999	CESP: F40F8.5	; 422/2; 440/3;); 1; Gaps 1;
RESULT 1 T22033 hypothetical protein F40F8.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Stete: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct-1999 C;Accession: T22033 R;MacDougall, R. Submitted to the EMBL Data Library, February 1996 A;Reference number: Z19505 A;Accession: T22033	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-879 < WIL> A;Cross-references: EMBL:269302; PIDN:CAA93261.1; GSPDB:GN00020; CESP:F40F8.5 A;Experimental source: clone F40F8 C;Genetics: A;Gene: CESP:F40F8 A;Gene: CESP:F40F8 A;Gene: CESP:F40F8	A;Map position: 2 A;Introns: 63/1; 149/1; 173/1; 217/1; 262/1; 306/1; 347/1; 381/2; 422/2; 440/3;	Ouery Match 43.5%; Score 60.5; DB 2; Length 879; Best Local Similarity 52.2%; Pred. No. 1.4; Matches 12; Conservative 5; Mismatches 5; Indels

461/3

5 TNKSEK-AERKSHDTQTTQEICE 26 3 TNKREKQLERECHEQKTSQAVCE δλ g

Accession: S48320
Accession: S18898
Accession: S18989
Accession: S1898
Accession: S1888
Accession: S1



Patent No. US20010029295A1

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Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 677;
                                                               APPLICANT: Sleath, Paul R.
APPLICANT: MCNell1, Patricia D.
APPLICANT: MCNell1, Patricia D.
APPLICANT: MCNELLID, Patricia D.
APPLICANT: Compounds AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS FILE REFERENCE: 210121.426C9
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 1444
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Moweill, Patricia D.
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: APPLICANT: APPLICANT: SECRISTILE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION FILE REFERENCE: 210121.426C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 139; DB 10; 100.0%; Pred. No. 7.8e-12;
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/853,079 CURRENT FILING DATE: 2001-05-09
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                                             Houghton, Raymond L.
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Houghton, Raymond L.
Reed, Steven G.
Lodes, Michael J.
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Best Local Similarity 100.
Matches 26; Conservative
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Matches 26; Conserv
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; APPLICANT: Reed, St
; APPLICANT: Lodes, M
; APPLICANT: Houghton
                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
ORGANISM: Babesia
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US-09-853-079-87
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                                                                                                                                                       APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: McNelll, Patricia D.
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILLE REFERENCE: 210121.426211
CORRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
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Best Local Similarity 100.0%; Pred. No. 7.8e-12;
Matches 26; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 144
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CURRENY PAPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
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US-09-737-178-144
; Sequence 144, Application US/09737178
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Publication No. US20030109689A1
GENERAL INFORMATION:
                                          Sequence 85, Application US/09737178 Patent No. US20010029295A1
                                                                                                               Reed, Steven G.
Lodes, Michael J.
Houghton, Raymond L.
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Best Local Similarity 100.
Matches 26; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: PRT
; ORGANISM: Babesia
US-09-737-178-85
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US-09-853-079-144
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                    US-09-737-178-85
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TYPE: PRT

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APPLICANT: Boughton, Raymond L.
APPLICANT: Boughton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Moneil, Paul R.
APPLICANT: Moneil, Patricia D.
APPLICANT: Scrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C11
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
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  Indels
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    0; Mismatches
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                                        218 GKPNTNKSEKAERKSHDTQTTQEICE 243
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CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
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                                                                                                                                                                                   ; Sequence 211, Application US/09853079; Publication No. US20030109689A1
; RENERL INFORMATION: APPLICANT: Reed, Steven G.
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APPLICANT: McNeill, Patricia D.
APPLICANT: Homer, Mary
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Best Local Similarity 100.
Matches 26; Conservative
  26;. Conservative
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Best Local Similarity
Matches 26; Conserva
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US-09-853-079-85
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APPLICANT:
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APPLICANT: Sleath, Paul R.

APPLICANT: McNeill, Particia D.

APPLICANT: Homer, Mary

APPLICANT: Secrist, Heather

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION

FILE REFERENCE: 210121.42669

CURRENT APPLICATION NUMBER: US/09/737,178

CURRENT FILING DATE: 2000-12-13

NUMBER OF SEQ ID NOS: 144

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                                                           Length 445;
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                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Lodgs, Michael J.
APPLICANT: Lodgs, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Mowell, Paul R.
APPLICANT: Homer, Mary
APPLICANT: Secrist, Mary
APPLICANT: Secrist, CHOHONIS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: CAND TREATMENT OF B. MICROTI INFECTION
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                                                         100.0%; Score 139; DB 9;
100.0%; Pred. No. 4.9e-12;
tive 0; Mismatches 0;
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Pred. No. 4.9e-12;
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Local Similarity 100.0%; Pred. No. 4.9
hes 26; Conservative 0; Mismatches
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CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001.05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                  182 GKPNTNKSEKAERKSHDTQTTQEICE 207
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                                                                                                                                                                                                                                                                                     Sequence 38, Application US/09853079
Publication No. US20030109689A1
GENERAL INFORMATION:
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100.0%;
                                        Query Match
Best Local Similarity 100.v
; ORGANISM: Babesia microti
US-09-286-488-38
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US-09-737-178-38
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Best Local Similarity
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US-09-853-079-38
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APPLICANT: Sleath, Paul R.
APPLICANT: Movelil, Paul R.
APPLICANT: Movelil, Paul R.
APPLICANT: Movelil, Paul R.
APPLICANT: Gerist, Heather
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REPERENCE: 210121.42669;
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT APPLICATION NUMBER: US/09.737,178
SOFTWARE: FASTSEQ for Windows Version 3.0
SOFTWARE: FASTSEQ for Windows Version 3.0
TENGRAL 7.75
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                                                                                                                                                                                                                                                   Length 275;
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michel J.
APPLICANT: Lodes, Michel J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Moneill, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Moneill, Patricia D.
APPLICANT: Moneill, Patricia D.
APPLICANT: Moneill, Patricia D.
APPLICANT: MONEIL J. 1456
CURRENT APPLICATION NUMBER: US/09/286,488
CURRENT FILING DATE: 1999-04-05
                                                                                                                                                                                                                                                                                                       Indels
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Pred. No. 2.9e-12;
; Mismatches 0;
                                                                                                                                                                                                                                                      100.0%; Score 139; DB 9; 100.0%; Pred. No. 2.9e-12;
                                                                                                                                                                                                                                                                                                       0; Mismatches
                            CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 53
LENGTH: 275
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SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 38
LENGTH: 445
                                                                                                                                                                                                                                                                                                                                                                                 118 GKPNTNKSEKAERKSHDTQTTQEICE 243
       CURRENT APPLICATION NUMBER: US/09/853,079 CURRENT FILING DATE: 2001-05-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Sequence 38, Application US/09286488
; Patent No. US20020169136A1
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                                                                                                                                                                                                                                                                             Best Local Similarity 100.
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Reed, Steven G.
                                                                                                                                                       ; TYPE: PRT
; ORGANISM: Babesia microti
US-09-853-079-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; ORGANISM: Babesia microti
US-09-737-178-53
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Best Local Similarity
Matches 26; Conserva
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APPLICANT: Reed, S
APPLICANT: Lodes, 1
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US-09-737-178-53
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APPLICANT: Sleath, Paul R.

APPLICANT: Momeill, Patricia D.
APPLICANT: Homer, Mary
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS NUMBER: US/09/853,079
CURRENT APPLICATION NUMBER: 105/09/853,079
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 194
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 53, Application US/09286488
Patent No. US20020169136A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: McNelll, Patricia D.
TITLE OF INVENTION: AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TRAATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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1larity 100.0%; Pred. No. 2.9e-12;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                DB 9;
                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
100.0%; Score 139; Dest Local Similarity 100.0%; Pred. No. 4.3
Matches 26; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/286,488 CURRENT FILING DATE: 1999-04-05 NUMBER OF SEQ ID NOS: 83 SOFTWARE: PASLSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sleath, Paul<sup>*</sup>R.
APPLICANT: MCNelll, Patricia D.
APPLICANT: HOMEr, MATY
APPLICANT: Secrist, Heather
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Babesia microti
US-09-286-488-53
                                                                                                                                                                                                                                                                                                                           ; TYPE: PRT
; ORGANISM: B. microti
US-09-853-079-194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 26; Conserv
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LENGTH: 275
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Sequence 39, Appl Sequence 39, Appl Sequence 5866, Ap

US-09-853-079-39 US-09-737-178-39 US-10-106-698-5866

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July 16, 2003, 17:47:39; Search time 4.25295 Seconds (without alignments) 726.026 Million cell updates/sec
GenCore version 5.1.6 Copyright (c) 1993 - 2003 Compugen Ltd.
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                                                                                             OM protein - protein search, using sw model
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Total number of hits satisfying chosen parameters: 451899 seqs, 118759770 residues BLOSUM62 Gapop 10.0 , Gapext 0.5 Minimum DB seq length: 0 Maximum DB seq length: 2000000000 Searched:

Scoring table:

Sequence:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Sequence 195, App Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 53, Appl Sequence 38, Appl Sequence 38, Appl Sequence 85, Appl Sequence 85, Appl Sequence 85, Appl Sequence 87, Appl Sequence 87, Appl Sequence 87, Appl Sequence 87, Appl Description US-09-853-079-195 US-09-853-079-194 US-09-853-079-53 US-09-853-079-53 US-09-853-079-83 US-09-853-079-38 US-09-853-079-38 US-09-853-079-38 US-09-853-079-88 01000100100 Query Match Length DB 481 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 45.3 Score Result

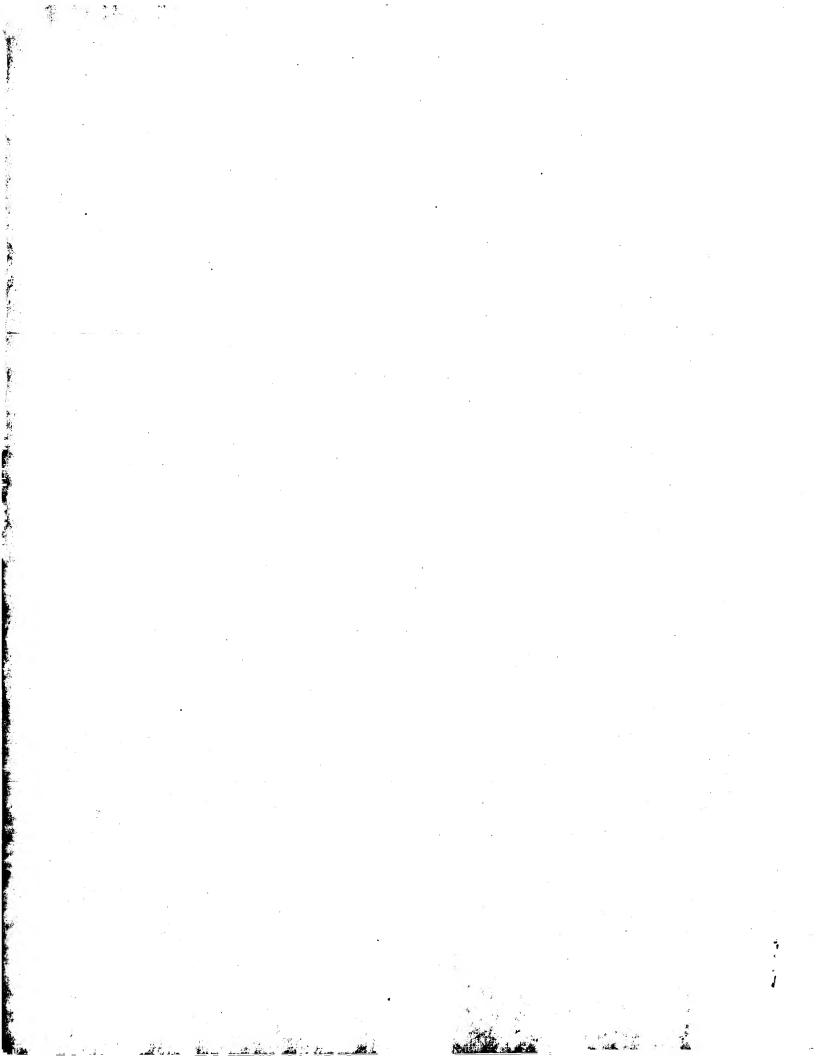
Sequence 201, App Sequence 197, App Sequence 192, App Sequence 39, Appl

US-09-737-178-87 US-09-853-079-201 US-09-853-079-197 US-09-853-079-192 US-09-286-488-39

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US-09-853-079-202 US-09-853-079-202 US-09-853-079-202 US-09-925-300-132: US-10-176-758-542 US-10-176-758-542 US-10-175-738-542 US-10-175-738-542 US-10-175-738-542 US-10-175-738-542 US-10-176-758-542 US-10-176-758-542 US-10-176-757-542 US-10-176-757-542 US-10-176-757-542 US-10-176-757-542 US-10-176-757-542 US-10-176-757-542 US-10-176-757-542 US-10-174-572-542 US-10-174-572-542 US-10-174-572-542 US-10-174-573-542 US-10-174-573-542 US-10-174-573-542 US-10-174-573-542 US-10-174-573-542 US-10-176-773-542	ALIGNMENTS BESULT 1 1S-09-853-079-195 Sequence 195, Application US/09853079 Publication No. US20030109689A1 GENERAL INFORMATION: APPLICANT: Reed, Stewen G. APPLICANT: Lodes, Michael J. APPLICANT: Adventor, Raymond L. APPLICANT: Aleath, Paul R. APPLICANT: Mary Expericant: Mary APPLICANT: Mary Computor Momer, Mary APPLICANT: Action Compounds APPLICANT: Secrist, Heather TILLE OF INVENTION: COMPOUNDS AND METHODS FOR TILLE OF INVENTION: AND TREATMENT OF B. MIC FILE REFERENCE: 21012.1.426C11 CURRENT PILLING DATE: 2001-05-09 NUMBER OF SEQ ID NOS: 224 CURRENT FILLING DATE: 2001-05-09 NUMBER OF SEQ ID NOS: 224 LENGTH: 26 TYPE FREE FASTEED for Windows Version 3.0 SOFTWARE: FASTEED for Windows Version 3.0 CORGANISM: B. microti	Score 139; Pred. No. 2. Mismatches TOEICE 26 HIHH TOEICE 26
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	ALIGNMENT 079 METHODS 7653,079	ore 1 ed. N Misma Misma ICE 2 ICE 2
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	AL 985307 L. D. S/09/8	imilarity 100 0%; Score conservative 0; Miss GKPNTNKSEKAERKSHDTQTTQEICE [
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200 200 200 200 200 200 200 200 200 200	Application US/098 Application US/098 MATION: Ged, Steven G. Lodes, Michel J. Houghton, Raymond L. Steath, Paul R. MCHILL, Patricia D. Homer, Mary Secrist, Heather ENTION: COMPOUNDS A. ENTION: COMPORER: US/ OLD NOS: 224 StSEQ for Windows V.	10 10 10 10 CAERK (AERK (AERK) (1111 (AERK) (1010) (1010) (1010)
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00000000000000000000000000000000000000	ESULT 1 S-09-853-079-195 Sequence 195, Applica Publication No US20/ GEMERAL INFORMATION: APPLICANT: Houghton APPLICANT: Secrist TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION CURRENT APPLICATION CURRENT APPLICATION CURRENT FILING DATE NUMBER OF SEQ ID NOG SOFTWARE: FastSEQ fG SEQ ID NO 195 LENGTH: 26 TYPE: PRF CREATER APPLICANTION: TYPE	Query Match Best Local Similarity 100.0%; Matches 26; Conservative 0; Oy 1 GKPNTNKSEKAERKSHDTOTT
, w 4 N O C B O O C C W 4 N O C B O O C C C W 4 N	SSULT 1 5-09-853-079- Sequence 199 Publication GENERAL INFR APPLICANT: APPLICANT: APPLICANT APPLICANT APPLICANT TITLE OF INTILE OF INTIL	Query Match Best Local S Matches 26 1 1 1 SSULT 2 Sequence 194 Publication GENERAL INPO GENERAL INPO APPLICANT: APPLICANT:
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Sequence 7, Application US/08841349B
Fatent No. 5955594
GENERAL INFORMATION:
TITLE OF INVENTION: GENES CODING PROTEINS FOR EARLY LIVER DEVELOPMENT.
FILLE REFERENCE: XX/PO4470US0
CURRENT APPLICATION UNDMER: US/08/841,349B
CURRENT FILING DATE: 1997-04-30
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              33.8%; Score 47; DB 2; Length 220; 37.5%; Pred. No. 11;
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Job time: 3.36762 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CORGANISM: Mus musculus
US-08-841-349-7
                                                                                                                 US-08-841-349-7
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APPLICANT: BOLIACK-SJOGIN, Ann
APPLICANT: BOTAGATION:
APPLICANT: BOTAGATION:
APPLICANT: Cole, Philip
APPLICANT: Cole, Philip
APPLICANT: Culyan, John
TITLE OF INVENTION: THEREOF
FILE REFERENCE: 600-1-228N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 45.3%; Score 63; DB 4; Length 32; Best Local Similarity 63.6%; Pred. No. 0.0046; Matches 14; Conservative 0; Mismatches 8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: VARIANT
LOCATION: (27)...(27)
OTHER INFORMATION: Xaa - Cysteine or Serine
NAME/KEY: VARIANT
LOCATION: (28)...(28)
OTHER INFORMATION: Xaa - Aspartic Acid or Glutamic Acid
NAME/KEY: VARIANT
                                                                                                                 NAME/KEY: VARIANT
LOCATION: (14)...(14)
OTHER INFORMATION: Xaa = Glutamic Acid or Glycine
NAME/KEY: VARIANT
                   OTHER INFORMATION: Xaa = Glutamic Acid or Glycine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: (29)...(29)
OTHER INFORMATION: xaa = Glutamic Acid or Alanine
                                                                                                                                                                             LOCATION: (15)...(15)
OTHER INFORMATION: Xaa = Isoleucine or Arginine NAME/KEY: VARIANT
LOCATION: (18)...(18)
OTHER INFORMATION: Xaa = Histidine or Tyrosine NAME/KEY: VARIANT
LOCATION: (18)...(18)
                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (26)...(26)
OTHER INFORMATION: Xaa = Isoleucine or Threonine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: VARIANT

LOCATION: (30)...(30)

CHER INFORMATION: Xaa = Cysteine or Histidine
US-09-528-784A-39
                                                                   LOCATION: (12)...(12)
OTHER INFORMATION: Xaa = Lysine or Asparagine
                                                                                                                                                                                                                                                                                                                                               LOCATION: (23)...(23)
OTHER INFORMATION: Xaa = Threonine or Proline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/356,952
CURRENT FILING DATE: 1999-07-19
EARLIER APPLICATION NUMBER: 60/093,631
BARLIER FILING DATE: 1998-07-21
NUMBER OF SED ID NOS: 14
SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 KPNTNKSEKAERKSHDTQTTQE 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4 KXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Saccharomyces cerevisiae US-09-356-952-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09356952
Patent No. 6117663
                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: VARIANT
                                                VARIANT
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Paul R. COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. MICROTI INFECTION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Residue can be either Gly or Asp"
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or Ile"
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or Arg"
                                                                                                                                                                                  ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPARE: Patentin Felease #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,142A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Residue can be either or Gly"
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                                                                                            ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Residue can be
                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
RECESTENCE/DOCKET NUMBER: 210121.426
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 39: SEQUENCE CHARACTERISTICS: LENGTH: 32 amino acids TYPE: amino acids STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "
or Thr"
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LOCATION: 3
OTHER INFORMATION: /note-
OTHER INFORMATION: or Asp'
FEATURE:
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LOCATION: 5
O'THER INFORMATION: /note-
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FEATURE:
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NAME/KEY: Modified-site
LOCATION: 14
OTHER INFORMATION: /note=
OTHER INFORMATION: or Gly
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NAME/KEY: Modified-site
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                                                        NUMBER OF SEQUENCES: 49
                                                                                                               STREET: 6300 Columb
CITY: Seattle
STATE: Washington
COUNTRY: USA
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OTHER INFORMATION:
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OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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APPLICANT: Sleath, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
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GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Gleath, Paul R.
APPLICANT: Modelil, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TORREW FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
LENGTH: 32
                                    OTHER INFORMATION: /note= "Residue can be either Thr OTHER INFORMATION: or Pro"
FEATURE: NAME/KEY: Modified-site
LOCATION: 26
OTHER INFORMATION: Or Thr"
FEATURE:
NAME/KEY: Modified-site
COTHER INFORMATION: Or Thr"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 27
OTHER INFORMATION: /note= "Residue can be either Cys OTHER INFORMATION: or Ser"
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8; Indels
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or Ala"
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or Glu"
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OTHER INFORMATION: Xaa = Glycine or Aspartic Acid
NAME/KEY: VARIANT
LOCATION: (5)...(5)
OTHER INFORMATION: Xaa = Proline or Isoleucine
NAME/KEY: VARIANT
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Pred. No. 0.0046;
0; Mismatches
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OTHER INFORMATION: Xaa = Lysine or Threonine
NAME/KEY: VARIANT
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Patent No. 6451315
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LOCATION: 28
OCHER INFORMATION: Or Glu'
FEATURE:
NAME/KEY: Modified-site
LOCATION: 29
OTHER INFORMATION: /note=
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| LOCATION: 30

| OTHER INFORMATION: /note

| OTHER INFORMATION: or Hi

US-08-723-142A-39
Modified-site
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Best Local Similarity 63.6'
Matches 14; Conservative
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ORGANISM: Babesia microti
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                                       /note= "Residue can be either Glu or Gly"
                                                                                                                                                 /note= "Residue can be either Lys
or Asn"
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OTHER INFORMATION: /note= "Residue can be either lle
OTHER INFORMATION: or Arg"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 18
OTHER INFORMATION: or Tyr"
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or Thr"
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NAME/KEX: Modified-site
LOCATION: 27
OTHER INFORMATION: /note= "Residue can be either Cys
OTHER INFORMATION: or Ser"
NAME/KEY: Modified-site
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or Ala"
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or Glu"
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Patent No. 6306396
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
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NAME/KEY: Modified-site
LOCATION: 23
  Modified-site
                                                                                                                Modified-site
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OTHER INFORMATION: OTHER INFORMATION: FEATURE:
NAME/KEY: Modified-s
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OTHER INFORMATION:
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COTHER INFORMATION:
US-08-990-571-39
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OTHER INFORMATION:
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US-08-723-142A-39
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APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B. M
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
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Pred. No. 0.0046;
0; Mismatches 8; Indels
                                              /note= "Residue can be either Glu
or Ala"
                                                                                                                                                        OTHER INFORMATION: /note= "Residue can be either Cys; OTHER INFORMATION: or His" GS-08-845-258-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTE: 70104
COMPUTE: FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
CLESSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                    4 KXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                          2 KPNTNKSEKAERKSHDTQTTQE 23
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INFORMATION FOR SEQ ID NO: 39:
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 63.6%;
Matches 14; Conservative
                                                                                                              NAME/KEY: Modified-site LOCATION: 30
Modified-site
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NAME/KEY: Modified-
LOCATION: 29
OTHER INFORMATION:
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OTHER INFORMATION:
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CITY: Seattle
STATE: Washington
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ZIP: 98104
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LOCATION:
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                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; DB 4; Length 1132;
8.3e-13;
hes 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: SED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                      JAPPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Bloughton, Raymond L.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C4
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT PILLICATION NUMBER: US/09/528,784A
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FEASTSEQ for Windows Version 3.0
                                                                      Query Match
100.0%; Score 139; DB 4; Length 666;
Best Local Similarity 100.0%; Pred. No. 4.5e-13;
Matches 26; Conservative 0; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 139; I
Best Local Similarity 100.0%; Pred. No. 8.3
Matches 26; Conservative 0; Mismatches
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FILING DATE: 24-APR-1997
                                                                                                                                                                                                                                                                                                                                         Sequence 87, Application US/09528784A Patent No. 6451315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-845-258-39; Sequence 39, Application US/08845258; Patent No. 6183976
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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US-09-528-784A-87
; ORGANISM: Babesia
US-09-528-784A-85
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LENGTH: 1132
TYPE: PRT
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/note- "Residue can be either Gly or Asp"
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or Thr"
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or Asn"
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or Thr"
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or Ser"
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or Glu"
                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "Residue can be either Pro OTHER INFORMATION: or Ile"
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or Gly"
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or Arg"
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NAME: Maki, David J.
REGISTRATION NUBBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-4900
SEGUENCE CHARACTERISTICS:
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LOCATION: 12
OTHER INFORMATION: /note-
OTHER INFORMATION: or Asn'
FEATURE:
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NAME/KEY: Modified-site
LOCATION: 5
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NAME/KEY: Modified-site
LOCATION: 7
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14
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23
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28
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FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
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                                                                                                                             LENGTH: 32 amino acids TYPE: amino acid STRANDEDNESS:
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OTHER INFORMATION:
OTHER INFORMATION:
FEATURE:
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LOCATION: 18
OTHER INFORMATION:
OTHER INFORMATION:
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NAME/KEY: Modified
LOCATION: 23
OTHER INFORMATION:
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OTHER INFORMATION:
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NAME/KEY:
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NAME/KEY:
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Gaps
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Fatent No. 6451315

GENERAL INFORMATION:
APPLICANT: Redes, Steven G.
APPLICANT: Bodes, Michael J.
APPLICANT: Blath, Paul R.
APPLICANT: Glath, Paul R.
APPLICANT: McNeill. Patricia D.
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFRENCE: 210121.42664
CURRENT APPLICATION NUMBER: US/09/528,784A

CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 38
LENGTH: 445
                                                                                                                                                                                                                                                                                                                                                                                                  Length 445;
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APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Moneill, Pauricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATHENT OF B. MICROTI INFECTION
FILLE REPERENCE: 210121.4264
CURRENT PRILING DATE: 2000-03-17
SUTRENT FILING DATE: 2000-03-17
SUTRENT FILING DATE: 2000-03-17
SUTRENT FILING DATE: 2000-03-17
SUTRENT FILING DATE: 2000-03-17
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   REFERENCE/DOCKET NUMBER: 210121.426
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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                                 TELECOMMUNICATION INFORMATION TELEPHONE: (206) 622-4900
                                                                                          TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 100.0
Matches 26; Conservative
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Matches 26; Conservative
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APPLICANT: Reed, Steven G.
                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                               STRANDEDNESS
                                                                                                                                                                                                                                                                                                    ; TOPOLOGY:
US-08-723-142A-38
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Patent No. 6306396
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Bleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION COMPOUNDS AND ADDRESSED OF B. MICROTI INFECTION COMPOUNDS ADDRESSED OF B. MICROTICAL COMPOUNDS ADDRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 445;
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                                                                                                                                                                                                                                              ZIP: 98104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
                                                                                       ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 139; DB 4;
100.0%; Pred. No. 2.8e-13;
Live 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C2
REFERENCAMUNICATION INFORMATION:
TELECHOME: (206) 622-4900
TELEFAX: (206) 682-6031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   182 GKPNTNKSEKAERKSHDTQTTQEICE 207
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CLASSIFICATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MBER: US/08/990,571
11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MAK1, DAVIG J. 1,392
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 38:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.0
Matches 26; Conservative
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APPLICATION NUMBER: US,
                                 NUMBER OF SEQUENCES: 7: CORRESPONDENCE ADDRESS:
                                                                                                                            Start: Seattle STATE: Washington COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear
US-08-990-571-38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1 CLASSIFICATION:
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
ITILE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                            Length 275;
                                                                                                                                                                   Indels
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APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTONNEY/AGERT INFORMATION:
NAME: MAKI, DAVIG J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 2.0121.426C1
TELECOMMULCATION INFORMATION:
TELECOMMULCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6300 Columbia Center, 701 Fifth Avenue
                                                                                                                          Query Match 100.0%; Score 139; DB 4; Best Local Similarity 100.0%; Pred. No. 1.6e-13; Matches 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                    218 GKPNTNKSEKAERKSHDTQTTQEICE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                      Sequence 38, Application US/08845258 Patent No. 6183976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Reed, Steven G. et al
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; Sequence 38, Application US/08990571
; Patent No. 6214971
; GENERAL INFORMATION:
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ilarity 100.0%;
Conservative 0;
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                                         TYPE: PRT
ORGANISM: Babesia microti
US-09-528-784A-53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Seattle
STATE: Washington
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Best Local Similarity
Matches 26; Conserva
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SEQ ID NO 53
LENGTH: 275
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                                                                                                                                           Sequence 53, Application US/08990571
Patent No. 6214971
GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et al.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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APPLICANT: Sleath, Paul R.
APPLICANT: MCNE111, Pauticia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROIL INFECTION
FILE REFERENCE: 210121,426C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPPERTYING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
RPPLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                          6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; Score 139; DB 4; Similarity 100.0%; Pred. No. 1.6e-13; 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 210121.426C2 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/528,784A CURRENT FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
                          218 GKPNTNKSEKAERKSHDTOTTOEICE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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Sequence 53, Application US/09528784A
Patent No. 6451315
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Houghton, Raymond L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (206) 622-4900
TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                             SEED AND BERRY
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amino acid
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CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104
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Best Local Similarity
Matches 26; Conserv
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                                                                                                                       US-08-990-571-53
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GenCore version 5.1.6

Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 16, 2003, 17:42:54; Search time 2.36762 Seconds

(without alignments)
323.107 Million cell updates/sec

Title: US-09-853-079-195
Sequence: 139
Sequence: 1 GENPURNSERAERKSHDTQTTQEICE 26
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 262574 seqs, 29422922 residues
Total number of hits satisfying chosen parameters: 262574
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Listing first 45 summaries
Database : Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PaCMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PaCMB.pep:*
6: /cgn2_6/ptodata/1/iaa/PaCMF.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 85, Appl Sequence 87, Appl Sequence 39, Appl Sequence 39, Appl Sequence 39, Appl Sequence 5, Appli Sequence 7, Appli Sequence 13, Appli Sequence 113, Appli Sequence 110, Appli Sequence 53, Sequence 38, Sequence 38, Sequence 38, Sequence 38, Sequence 87, Sequence 87, Sequence 39, Seque Sequence 53, Description Sequence 1 Sequence 8 Sequence 3 Sequence US-08-845-258-53 US-08-990-571-53 US-08-990-571-53 US-08-990-571-38 US-08-990-571-38 US-09-528-784A-85 US-09-528-784A-85 US-09-528-784A-87 US-08-990-571-39 US-08-990-571-39 US-09-958-784A-87 US-08-990-571-39 US-09-958-784A-39 US-09-958-784A-39 US-09-958-784A-39 US-09-95-784A-39 US-09-185-160-9 US-09-185-160-9 US-09-185-160-13 US-09-185-160-13 US-09-199-955-10 US-09-199-955-10 US-08-199-955-10 US-08-199-955-10 US-08-191-055-10 US-08-1131-6258-17 US-08-1131-6258-17 US-08-1131-6258-17 US-08-1131-6258-17 US-08-1131-6258-17 US-08-1131-6258-17 SUMMARIES Length DB 445 445 666 1132 32 32 32 10048 2120 2120 2154 259 259 3433 3433 3433 1123 534 576 Query Match I 1000.0 10000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1000.0 1 Score 1139 921139 921139 921139 921139 92139 92139 92139 92139 92139 Š.

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Gaps

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Length 275; Indels

Query Match. 100.0%; Score 139; DB 4; Best Local Similarity 100.0%; Pred. No. 1.6e-13; Matches 26; Conservative 0; Mismatches 0;

TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:

STRANDEDNESS: single

Babesia Microti

; ORGANISM: US-08-845-258-53

Sequence 3517, Ap Sequence 11, Appli Sequence 2, Appli Sequence 5080, Ap Sequence 37, Appli Sequence 26, Appli Sequence 26, Appli Sequence 27, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 12, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 6, Appli Sequence 6, Appli Sequence 6, Appli		DIAGNOSIS
9 652 4 US-09-134-001C-3517 9 752 1 US-09-244-189-2 9 3696 4 US-09-134-001C-5080 245 4 US-09-134-001C-5080 2461 2 US-08-463-587A-26 461 2 US-08-463-587A-26 461 2 US-08-463-587A-26 461 2 US-08-463-587A-26 461 2 US-08-463-587A-26 461 3 PCT-US91-09133-27 2 546 4 US-09-352-990-2 2 588 2 US-08-419-12 588 4 US-08-419-12 588 5 PCT-US93-07189-12 588 5 PCT-US93-07189-12 1566 2 US-08-296-23 1848 6 PCT-US93-07189-12 1848 5 PCT-US95-10661A-6 123 2 US-08-799-464A-13	ALIGNMENTS	T 1 -845-258-53 uence 53, Application US/08845258 uence 53, Application US/08845258 uence 53, Application US/08845258 uence 53, Application US/08845258 uence 53, Application APPLICANT: Lodes, Michael J. APPLICANT: Lodes, Michael J. APPLICANT: Lodes, Michael J. APPLICANT: Sleath, Paul R. TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOS TITLE OF INVENTION: ADD TREATMENT OF B. MICROTI INFECTION UNMBER OF SEQUENCES: 53 CORRESPONDENCE ADDRESS: ADDRESSEE: SED AND BERRY STREET: 6300 Columbia Center, 701 Fifth Avenue COUNTRY: USA ZIP: 98104 ZIP: 98104 ZOMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, Version #1.30 CLASSIFCATION NOTHER: 13,392 RECIFERATION HUMBER: 210121.426C1 TELENCATION NUMBER: 210121.426C1 TELECOMMUNICATION INFORMATION: REFERENCE/DOCKET NUMBER: 210121.426C1 TELECOMMUNICATION INFORMATION: LENGTH 275 amino acids TYPE: ILENGTH 275 amino acids TYPE: APPLICATION acids
		1 45-258-53 Application t No. 6183976 EAL INFORMATION: PLICANT: Reed, Stev PLICANT: Lodes, Mc PLICANT: Sleath, Pa TLE OF INVENTION: TLE OF INVENTION: TLE OF INVENTION: AMBER OF SEQUENCES: REESPONDENCE ADDRESS ADDRESSEE: 6300 Columb STREET: 6300 Columb STREET: 6300 Columb STREET: Washington COUNTRY: USA ADDRESSEE: BASHINGTON STREET: Washington COUNTRY: Washington COUNTRY: Gastle COUNTRY: USA STREET: 44-APR COMPUTER: LBM PC CO COMPUTER: LBM PC CO COMPUTER: LBM CC COMPUTER: LBM CC COMPUTER: LBM CC CORPUTER: LBM CC
2008 3300 3300 3300 3300 3300 3300 3300		RESULT 1 US-08-845-258-53 Sequence 53, Application US, Patent No. 6183976 GENERAL INFORMATION: APPLICANT: Reed, Steven APPLICANT: Reed, Michala PPLICANT: Codes, Michala PPLICANT: SLeath, Paul TITLE OF INVENTION: COMTITLE OF INVENTION: COMTITLE OF INVENTION: AND NUMBER OF SEQUENCES: 53 CORRESPONDENCE SEED AND B STREET: 6300 Columbia CITY: Seattle STARE: Washington CONFOUTER: IBM PC COMPOUTER: TEM PC COMPOUTER: TEM PC COMPOUTER: PASSIFICATION DATA APPLICATION NUMBER: DELING SYSTEM: A 55 ATTORNEY ABOUT ON UNDER: CLASSIFICATION NUMBER: UF LILING DATE: 24-APR-1 CLASSIFICATION NUMBER: UF LECOMMUNICATION INFORMATION NUMBER: REFERENCE/DOCKET NUM
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VPDEILSQKSPKFAIRHTATGIISHVDSAAVSALGYLPQDLIGRSIMDFYHHEDLSVMKE 438	IXHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGARSEGN 185 	NMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDG 237 :	YDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKA 282 	FDECKSNAIILKKKILDNDEDYKINFREWVNEVTCA 318 : :	NTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAV-TVSVSATSNGT 377 : :	ESG-GAGSGTGTSV-SATSTLTGNG-GTESGGTAGTTTSS	NDEMEKFMLKKHRESRGRTGEKSKKSANDTLKMLEYSGPGHGIKRGGSHSWEGEANKPKQ 832	TSGTTTSSGAASGKAG-TGTAGTTTSSEG-AGSDKAGTGTSGTTTSSGTGA-G 470 	GAGSGGPSGHASNA 484 	
VPDEILS(IYHTISS(: TYETVMKI	NMFQ : RVFQGPK(YDFDYING	FDE(: : PHHDYYD:	NTKFEAL) : SGASGPM	ESG-GAG : GTGTGTG	NDEMEKE	TSGTT QLTLGTD	GAGSGGP GAGGGGG	
379	129	186	238	283	319	378 713	415	421 _. 833	471	
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Search completed: July 16, 2003, 17:50:04 Job time : 125.145 secs

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Last sequence update)
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65; Mismatches 229;
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  Created)
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InterPro; IPR0010610; PAC.
InterPro; IPR000014; PAS_domain.
Pfam; PF00989; PAS; 2.
01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
                              PER protein.
PER OR EG:155E2.4 OR CG2647.
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Matches 139; Conserv
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 ---NREE 282
                                                                                 340 LTTEIDNNIEQISSY-----KSEITELRRNVQALE-----IELQSQLALKQSLEASL 386
                                                                                                                    356 TYIVGAGVEAVTVSVSATS-NGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSS 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTEAGGTSGT----TTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAG 470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          343 DVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGT 402
                                                                                                                                                                                           ESGGTAGTITSSGTEAGGTS----GTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGT 458
                                                                                                                                                                                                       173 FIEKLRGARSEGNNMFQEA-----LIRFRNASSEEMVNAASYLSAALFRYKEFDDE
                                       283 EMKHLRNVSTGDVNVEMNAAPGVDLTQLLNNMRN-QYEQLAEQNRKDAEAWFNEK--SKE
                                                              LFKKANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAF
                                                                                                       DECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKIN-R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Xiao L., Li L., Visvesvara G.S., Moura H., Didier E.S., Lal A.A.; "Genotyping Encephalitozoon cuniculi by Multilocus Analyses of Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 125;
LRQSVEADI ----NGLRRVLDELTLTQADLEMQIESLTEELAYLKK---
                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TTEMBLE-1.1), Last sequence update)
01-JUN-2002 (TTEMBLE-1.21, Last sequence update)
Spore wall protein-1 (Fragment).
Encephalitozoon cuniculi.
Eukaryota, Macrosporidia; Unikaryonidae; Encephalitozoon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      125 AA; 9983 MW; 30AE862B0D66643E CRC64;
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                                                                                                                                                                                                                                                525 GGGSSGGGYGGSSSGGHKSSSSGS 550
                                                                                                                                                                                                                                    SGTTTSSGTGAGGAGSGGPSGHASNA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     with Repetitive Sequences.";
J. Clin. Microbiol. 39:2248-2253(2001).
EMBL; AF340011; AAKG3051.1; -
PRINTS; PR01574; TUBBYPROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=USP A-2;
MEDLINE=21270266; PubMed=11376065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Conservative
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                                                             224
                                                                                                       284
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Q964C1;
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ID Q9W4X0
AC Q9W4X0;
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REDILING-20196005; PubMed=10731132;
RABADABEKELEY
RA Admas M.D. Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Admas M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA Admas M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Brandon R.C., Rogers Y.H.C., Blazef R.G., Champe M., Pfelifer B.D.,
RA Mari J.F., Apbayani A., Baxendale G., Hell G., Nelson C.R., Baldwin D.,
RA Abril J.F., Apbayani A., Baxendale J., Bayaktaroglu L., Bassley E.M.,
Beeson K.Y., Botchan M.R., Bouck J., Brokaten P., Bortcher P.,
Brokova D., Botchan M.R., Bouck J., Brokaten P., Bortcher P.,
RA Buris K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dalike C., Davaenport L.B., Davise P.,
RA Cherry J.M., Cawley S., Dalike C., Davaenport L.B., Davise P.,
RA Cherry J.M., Cawley S., Dalike C., Davaenport L.B., Davise S.,
R. Cherry J.M., Cawley S., Dalike C., Davaenport L.B., Davise S.,
R. Cherry J.M., Cawley S., Calbart W.M., Classer K.,
RA Cherry J.M., Cawley S., Barnes M. C.C., Ferraz C., Ferraz C., Ferras C., Ferras C., Gabriellan A.E., Gagg N.S., Dunkov B.C., Dunkov B.C.,
RA Adris N.J., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Rostler C., Gabriellan A.E., Gagg N.S., Calbart W.M., Calasser K.,
RA Haris N.J., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
Rostler C., Gabriellan A.E., Gagg N.S., Kalp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Linny Y., Lin X.,
Raktel B., McIncoh T.C., McLedd M.P., McSheel A.,
Raketel B., McIncoh T.C., McLedd M.P., McBron D.R.,
Raketel B., McIncoh T.C., McLedd M.P., McSheel A.,
Raketel B., McIncoh T.C., McLedd M.P., Shen G., Shue B.C., Stden Kiamos I., Shungon M., Strong R., Sun R.
Raketel R., Paraington K., Sauders R.D., Scheeler F., Shen H.,
Rabetel R., Remington K., Sauders R.D., Scheeler F., Shen H.,
Rabetel R., Spradling A.C., Sauders R.D., Scheeler F., Shen H.,
Rabeng X.H., Zhong F.N., Sundy W., Zhu S., Zhu X., Sanith H.O.,
Rheng X.H., Zhong F.N., 79 TPADV-AGVSDGFFIRGONLGAVGSVNE------QPNTVGMSLEQFIKNELYSFSNE 128 25 GEVTSNFRYISKEYEYEHTEL - - - - - AKEHCKKEKCVNVDNIEDNNLKIYAKQFKSVVT Drosophila melanogaster (Fruit fly). Eukaryota, Metazoa, Arthropoda, Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Length 1218; Indels SMART; SMO0086; PAC; 1. SMART; SM00091; PAS; 2. PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN_1. SEQUENCE 1218 AA; 127363 MW; 8506C15999F78AE3 CRC64;

us-09-853-079-52.rspt

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Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  493 GGGSAAAGGVSESSSGGSTAAGGTSESASGGSATAGGASGGTYTDSTGGSPTGSPSAGGP 552
                                                                                                                                                                                                                                 "Structural analysis of Arabidopsis thaliana chromosome 3. II.
Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genomic DMA, chromosome 3, BAC clone: T19N8.
Arabidopsis thaliana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-JUN-1998 (TIEMBLrel. 06, Last sequence update)
01-DEC-2001 (TIEMBLrel. 19, Last annotation update)
PGRS-family protein (Fragment).
RV3512 OR MIVO23.19.
Mycobacterium tuberculosis.
Mycobacterius tiemicutes; Actinobacterias Actinobacteriaes.
Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-98295987; pubMed-9634230; Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Coldon S.V., Eiglmeler K., Gas S., Barry C.E., III, Tekaia F., Badcook K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S. Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Stuter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the
                                                                                                                                              s:
                                                                                                                                                                                                                                                                                                                                                                 63;
                                                                                                                                                                                                                                                                                                                                      7.7%; Score 198.5; DB 10; Length 614; 33.5%; Pred. No. 0.048;
                                                                                                                                          Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                         360 GAGVEAVIVSVSAISNGT-ESGGAGSGTGTSVSA-ISTLIGNGGTESGG-
                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                            614 AA; 54412 MW; C522ADFC4062F06B CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          ---TAGTTTSSGTEAGGTSGT-TTSSGAASG-
                                                                                                                                                                                            STRAIN-COLUMBIA;
MEDLINE-20363099; PubMed-10907853;
                                                                                                                                                                                                                                                      TAC and BAC clones.",
DNA Res. 7:217-221(2000).
EMBL; AP002057; BAB03175.1;
HSSP; P41140; 25FA.
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                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                              STRAIN-COLUMBIA;
                                                                                         NCBI_TaxID=3702;
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360 GAGVEAVIVSVSATSNGTESGGAGSGTGTSVSATSTLT----GNGGTESGGTAGTTTSSG 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 79 T - - GGDGALAGSSGGAGGKGGNGGDAGKAGTGSAPGTAGTGGDGGKGGNGGIGAAGTTGP 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 DGGLLSGNEKVTMQNLNDRLASYLDKVRALEESNYELEGKIKERYDQHGNSRQGEPRDYS 190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 TEAGGTSGTTTSSGAA-----SGKAGTGTA-GTT-TSSEGAGSDKAGTGTSGTTTS 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GNGADNTTTAAAGTTGGAGGAGGAGGTGGTGGAAGTGTGGQQGNGG--NGGNGGTGGKGG 78
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDINE-89008465; PubMed-2459124; Zhou X.M., Idler W.W., Steven A.C., Roop D.R., Steinert P.M.; The complete sequence of the human intermediate filament chain feratin 10. Subdomainal divisions and model for folding of end domain sequences.";
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                  26;
                                                                                                                                                                                                                                                                                               Length 1079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                J. BLOJ. Chem. 263:15584-15589(1988).
-!- SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
EMBL; J04029; AAA60544:1; -.
InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                  81163 MW; A79718CDCB74B97D CRC64;
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:/ Intermediate
151 AA; 57247 MW; D647489FF26E157C CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                  57;
                                                                                                                                                 PROSITE; PS00318; HMG_COA_REDUCTASE_2; UNKNOWN_1
                                                                                                                                                                                                                                                                                        DB 16;
                                                                                                                                                                                                                                                                                                                    ; Pred. No. 0.095; 11; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        561 AA.
                                                                                                                                                                                                                                                                                        Score 198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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complete genome sequence.";
Nature 393:537-544(1998).
BMBL; AL022022; CAA17749.1; -.
Tuberculist; Rv3512; -.
InterPro; IPR002202; HMG-COA_red.
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                                                                                                                                                                                                                                                                                            7.78;
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TISSUE-FORESKIN EPIDERMIS;
                                                                                                                                                                                                                                                                                                                       Best_Local Similarity 37.7
Matches 57; Conservative
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Q964C4
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531 GGGRYGGGGSYGGSSGGGSSGGGSCGSYGGGSGG----GSYGGGSGGGSGGSHR 585
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-MANTLE;

MEDLINE-98070424; PubMed-9405458;

Shen X., Belcher A.M., Hansma P.K., Stucky G.D., Morse D.E.;

Shen X., Belcher A.M., Hansma P.K., Stucky G.D., Morse D.E.;

Molecular cloning and characterization of lustrin A, a matrix protein from shell and pearl nacre of Haliotis rufescens.";

J. Biol. Chem. 272:32472-32481(1997).

1. FUNCTION: PLAXS A STRCTURAL ROLE IN THE NACRE MATRIX FRAMEWORK OF THE SHELL. MAY ALSO PERFORM OTHER FUNCTIONS SUCH AS INTERACTING WITH POLYRANIONIC RARGONITE-DETERMINING PROTEINS, PROTECTING THE PROTEIN COMPONENTS OF THE MATRIX FROM DEGRADATION, AND CONFERRING ELASTIC RESILLENCE TO THE MICROLAMINATE COMPOSITE OF THE SHELL.

1- SUBSCELLULAR LOCATION: EXTRACELLULAR. SYNTHESIZED AND SECRETED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECIFICALLY BY THE MATTLE PALLIAL CELLS.
DOMAIN: THE PROTEIN CONTAINS TEN HIGHLY CONSERVED CYSTEINE-RICH
DOMAINS: THE PROTEIN CONTAINS TEN HIGHLY CONSERVED CYSTEINE-RICH
DOMAINS: THE SEGHT PROLINE-RICH DOMAINS. A GIYCINE-AND
SERINE-RICH DOMAIN LIES BETWEEN THE TWO CYSTEINE-RICH DOMAINS
NEAREST THE C TERMINAL AND THESE ARE FOLLOWED BY A BASIC DOMAIN
AND A C-TERMINAL DOMAIN THAT IS HIGHLY SIMILAR TO KNOWN PROTEASE
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Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda;
Haliotidae; Haliotis.
NCBI_TaxID=6454;
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N-LINKED (GLCNAC. ..)
N-LINKED (GLCNAC. ..)
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Last annotation update)
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HSSP; P19957; ZREL.
InterPro; IPR002221; WAP.
InterPro; IPR002899; WRL/EB.
PRINTS; PR00003; 4DISULPHCORE.
SWART; SW00217; WAP; 1.
SWART; SW00289; WRL; 4.
PROSITE; PS00317; 4_DISULFIDE_CORE; UNKNOWN_2.
Structural protein; Glycoprotein.
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GLY/SER-RICH.
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PRO-RICH.
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PRO-RICH.
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                                                                                                                                                                    PRELIMINARY;
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MEDLINE-21270266; PubMed=11376065;
MEDLINE-21270266; PubMed=11376065;
Xiao L. Li L., Visvesvara G.S., Moura H., Didler E.S., Lal A.A.;
"Genotyping Encephalitozoon cuniculi by Multilocus Analyses of Genes
with Repetitive Sequences."
J. Clin. Microbiol. 39:228-2253(2001).
EMBL; AF340008; AAK63048-11: --
PRINTS: PR01574; TUBBYPROTEIN.
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Eukaryota; Microsporidia; Unikaryonidae; Encephalitozoon.
NCBL_raxID=6035;
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01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
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Best Local Similarity 41.99
Matches 44; Conservative
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                                     ENFSDVNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMYNEV - TCANTKFEAL 325
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2001 (TrEMBLrel. 19, Last annotation update)
60-0CT-2001 (TrEMBLrel. 19, Last ann
                SAALFRYKEFDDELFKKANDNFGRDDGYDFDYINTKK-ELVI--LASVLDGLDLIMERLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; AP002057; BAB03182.1; -.
SEQUENCE 342 AA; 31165 MW; B78F9602BCD914A7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGTGTAGTTTSSEG--AGSDKAGTGT-SGTTTSSGTG-AGGAGSGGPSGHAS 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
0 day neonate head cDNA, RIKEN full-length enriched library,
clone:4833436C19, full insert sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      8.1%; Score 209; DB 10;
40.1%; Pred. No. 0.0081;
ative 24; Mismatches 57;
                                                                                                                                                                                                                506
                                                                                                                                                                        326 NDLIISDCEKKGIKINRDVISSYKLLLSTITY 357
                                                                                                                                                                                                                                                                                                                342 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      637 AA.
                                                                                                                                                                                                     EDITITICE ----KHNNPVLIRFSCSIEKYYY
                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-COLUMBIA;
MEDLINE-20363099; Pubmed-10907853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 40.1%
Matches 69; Conservative
                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eurosids II; Bra
NCBI_TaxID=3702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nakamura Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    323
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                                                                                          268
                                                                                                                                 428
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                                                                                                                                                                                                                                                                       RESULT 7
Q9LH90
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Rawai J., Shinagawa A., Shibata Y., Yoshino M., Itoh M., Ishii Y.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
Ra Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
Ra Rahl P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H.,
Ra Schriml L.M., Staubli F., Suzuki R., Tomita M., Ragner L., Washio T.,
Ra Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Ra Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
Ra Sakai K., Okido T., Fletcher C., Fujita M., Gariboldi M.,
Ra Uyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
Rotrone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Whyshaw Booris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
Wangachizaki V., Wang K., Rawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 GFGSGGGFGGGTFGSMGPVCPPGGIQEVTINQSLLQPLNVEVDPQIQKVKSQEREQIKSL 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  385 GTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTT 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            140 ----SFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGARSEGNNMFQEALIR 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   196 NDKFASFIDKV--RFLEQQNQVLQTKWELLQQVDT------TTRTQNLDPFFENYIS 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---- DVNNTDDIKKAFD 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | | : | | : | | : |: |305 TKVELQAKADAL----QQDIDFFSALYQMEMSQMQTQISETNVVLSMDNNRSLDLDGIIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECKSN-AIILKKKILDNDEDYKINFREMVNEVTCA-----NTKFE--ALNDLI----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----ISSYKLLLSTITYIVGAGVE------AVTVSVSATS-NGTESGGAGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  195 FRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDFDYINTKKEL----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       85 GVSDGFFIRGQNLGAVGSV----NEQPNTVGMSLEQFIKNELYSFSNEIYHTISSQISN-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              <del>::</del>
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-:
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 637;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match

8.1%; Score 207.5; DB 11;
Best Local Similarity 21.5%; Pred. No. 0.019;
Matches 110; Conservative 74; Mismatches 175;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           330 ----ISDCEKKGIKINRDV---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250 --VILASVLDGLDLIMERLIENFS----
                                                                                                                                                             STRAIN-C57BL/6J; TISSUE-HEAD;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PEGNI; PF00038; Filament; 1.
PRINTS; PR00341; PRION.
PRINTS; PR01248; TYPELKERATIN.
PRINTS; PR01276; TYPEZKERATIN.
PROSITE; PS00226; IF; UNKNOWN 1.
SEQUENCE 637 AA; 65627 MW; D65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR001664; IF.
Interpro; IPR0002957; Keratin_I.
Interpro; IPR003054; Keratin_II.
Interpro; IPR000817; Prion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nature 409:685-690(2001).
EMBL; AK019521; BAB31776.1; -.
MGD; MGI:96698; Krt2-1.
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SEQUENCE FROM N.A. STRAIN=MN1;
               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                483 NAKI 486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    249 VAKI 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Babesia microti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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                 δλ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'A SEQUENCE FROM N.A.
'A Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
'A Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
'A Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
'A Bowser L., Carnintor P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
'A Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koosema E.,
'A Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
'A Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
'A Shinozaki K., Davis R.W., Ecker J.K., Theologis A.,
'Shinozaki K., Davis R.W., Ecker J.K., Theologis A.,
'Shinozaki K., Davis R.W., Ecker J.K., Theologis A.,
'Shinozaki K., Davis R.W., Seki M., Shinn P., Southwick A.,
'Shinozaki K., Davis R.W., Schen J.J.,
'Shinozaki K., Davis R.W., Seker J.K., Theologis A.,
'Shinozaki K., Davis R.W., Seker J.K., Seke
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 GAGVEAVTVSVSATSNGTESG-GAGSGTGTSVSATSTLTGNGGTESG-GTAGTTTSSGTE 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   418 AGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGGP 477
                                                                                                                                                                                                                                                                                                                                                                               "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety Pl,
                                                                 SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Rounsley S.D., Lin X., Ketchum K.A., Phillips C.A., Brandon R.C.,
Tebhrmann J.L., White O., Kerlavage A.R., Adams M.D., Somerville C.R.,
Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Brassica napus (Rape).

Eukaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Brassica.

NCBL_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.1%; Score 234.5; DB 10; Length 705; 16.1%; Pred. No. 0.0011;
                                                                                                                                                                                                                                           Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    42; Indels
                                                                                                                                                                   Submitted (JUL-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                72473 MW; DC7F51FC0FD39C05 CRC64;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBL_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-MAX-2002 (TrEMBLrel. 20, Last annotation update)
Jasmonate inducible protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 680 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA Res. 7:217-221(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01419; Jacalin;
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                                                                                                                                                                                                                                                                                                                                                                                                                       and BAC clones.
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                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                       FROM N.A.
                                                                                                                                                                                                                           STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                           PubMed=10907853;
                                                                                                                                                                                                                                                                                                                           STRAIN-COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                 Nakamura Y.;
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                                                                                                                                                                                                                                                                                                       SEQUENCE
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P93658;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                         373 TSNGTESGGAGSGT-GTSVSATST-LTGNGGTESGGT-AGTTTSSGTEAGGTSGTTTSSG 429
                                                                                                                                                                                                                                                                                                                                                                                                                                            430 AASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGT-----GAGGAGSGGPSGHAS 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 DNIEDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGM--SLEQ 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| : |: |: |: |: |: 312 PVLIRFSCSIEKYYY--YFYSMNNTNKWNNHNLKYDNRFKEHSDKNGINYYEISAFKW 369
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --KHDN 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   264 SQQNEL-SHPNKIYK------IKFSDYIIEFDDDAKLTTIGTVEDITIYTCKHNN 311
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L.D., Benson D.R., Krause P.J., Reed S.G., Persing D.H.; "Serological expression cloning of novel immunoreactive antigens of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
NCBL_TaxID=5868;
                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
Geshi N., Brandt A.;
"Two jasmonate inducible proteins from Brassica napus seedlings homologous to myrosinase binding proteins and jacalin.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
HSSP; P18670; 13AC.
                                                                                                                                                                                                                                                                                                                                                 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;
                                                                                                                                                                                                                                                                                       8.4%; Score 216; DB 10; Length 680;
4.4%; Pred. No. 0.008;
ve 8; Mismatches 49; Indels 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 592;
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                                                                                                                                                                        Interpro; IPR001229; Jacalin_lectin.
Pfam; PF01419; Jacalin; 4.
SEQUENCE 680 AA; 69937 MW; 8CDOCF16C30CALE2 CRC64;
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17AF410231C431DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
Seroreactive antigen BMN1-8 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 FIKNELYSFSNEIYHTISSQISNSFLIMMSDAIV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 0.011;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Babesia microti.";
Infect. Immun. 68:2783-2790(2000).
EMBL; AF206251; AAF68244.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              592 AA; 70686 MW;
                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 44.4%;
Matches 55; Conservative 8
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DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 372
                                         DEDYKINFREMYNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG 360
                                                             :|: :|| ||: || ||: || ISS---KYKLLVDEISNKAYGTLEGPAADNFDHFRNIWKSIVLKDWFIYCDLLLQHLIYK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 TKEKNKLKKELEKC-----FPEQY-----SLMKKEELARIFDNAST-----
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Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----LKKEGEGCEQIYNYEFIEKLRGARSEGNNMFQEALIR-FRNASSEEMVNAASY
                                                                                                                                                AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAG
                                                                                                                                                                                                                                                                                                                                                                                                                     Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mohamath R., Reynolds L.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-20231818; PubMed-10768973;
Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L
Benson D.R., Krause P.G., Reed S.G., Persing D.H.;
"Serological expression cloning of novel immunoreactive antigens
Babesia microti.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Jasmonate inducible protein ISOLOG (Jasmonate inducible protein, myrosinase binding protein-like) (Putative jasmonate inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59;
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01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.3%; Score 239.5; DB 5;
29.3%; Pred. No. 0.00031;
11ve 50; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Infect. Immun. 68:2783-2790(2000).
EMBL; AF206245; AAF68236.1; ...
SEQUENCE 362 AA; 39988 MW; IB88DCFEF2BD5133
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                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                Seroreactive antigen BMN1-3.
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                                                                                                                                                                                                                                                                             PRELIMINARY;
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01-JUL-1997 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
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les 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=5868;
                                                                                                                                                                                                                                                                                                                                                                                                   Babesia microti
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T02004.4.
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  ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180
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                                                                                                                            DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN
                                                                                                                                                  DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG
                                                                                                                                                                                                                                   AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGG
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                                         RSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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NCBI_TaxID=5868;
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Last annotation update)
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Pred. No. 1.9e-93;
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Babesia microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
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EMBL; AF206246; AAF68238.1; -.
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99.5%;
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nes 417; Conservative
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09NIN9;
01-OCT-2000 (TEMBLE-1
01-OCT-2000 (TEMBLE-1
01-OCT-2000 (TEMBLE-1
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SEQUENCE
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Scoring table:

Searched:

Database

Perfect score:

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OM protein

Run on:

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08/293 ralstonia s
09uve7 yarrowia li
08/e91 saccharomyc
0964c5 encephalito
053559 mycobacteri
08viy9 mycobacteri
008294 saccharomyc
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Q48031 haemophilus
Q9W4m4 drosophilus
Q9W4m4 drosophila
018740 canis famil
Q8Y420 mycococus
085783 mycococus
085785 mycobacteri
Q918W1 mycoplasma
Q918W1 mycoplasma
Q918W1 mycoplasma
Q911m9 babesia mic
Q911m9 babesia mic
Q9Nim9 babesia mic
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Q8VIS mycobacteri
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Q9ninO babesia mic
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053552 mycobacteri
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NCBL_TaxID=5868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L.D. Benson D.R., Krause P.J., Reed S.G., Persing D.H.; "Serological expression cloning of novel immunoreactive antigens of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 2565; DB 5; Length 503; 100.0%; Pred. No. 5.2e-114; Live 0; Mismatches 0; Indels 0
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503 AA; 53831 MW; 0098D5DBF1BEF5AA CRC64;
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Last annotation update)
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                  0964C2
09NIN0
09VIX93
09VX293
0964C5
053559
08179
08179
08171
048031
09VX00
083552
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018740
08VX1
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Q969D4
Q9NIM9
Q8VK71
Q8VJ15
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MEDLINE=20231818; PubMed=10768973;
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Infect. Immun. 68:2783-2790(2000).
EMBL; AF206247; AAF68239.1; -.
HSSP; P00778; 1GBJ.
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Matches 503; Conservative
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SEQUENCE FROM N.A.
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Q9nin9 babesia mic
Q9nip1 babesia mic
004310 arabidopsis
P93658 brassica na
Q9nin3 babesia mic
091490 arabidopsis
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Q91197 arabidopsis
Q14664 homo sapien
Q964c1 encephalito
Q944x0 drosophila
Q61869 mus musculu
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Q964c4 encephalito
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848.513 Million cell updates/sec
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                                                                                                                                                                                                                                                         1 KRFNEHTDMNGIHYYYIDGS......AKIPGIMTLTLFALLTFIVN 503
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                                                                                                                                    July 16, 2003, 17:37:48 ; Search time 122.145 Seconds
                  GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                        671580 seqs, 206047115 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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004310
903458
00NIN3
09DZR8
044341
0964C4
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sp_invertebrate:*
sp_mammal:*
sp_mhc:*
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sp_vertebrate:*
sp_unclassified:*
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sp_phage:*
sp_plant:*
sp_rodent:*
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sp_bacteria:*
sp_fungi:*
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Maximum DB seq length: 200000000
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Match Length DB
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 Usage by and for commercial
              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                              357 YIVGAGVEAVTVSVSATSNGTESG-GAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                        416 TEAGGTSGTTTSSGAASGKA-----GTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTG 468
                                                                                                                                                                                                                                                                                                                                                                                                 7.1%; Score 182.5; DB 1; Length 5263;
36.7%; Pred. No. 0.092;
Live 15; Mismatches 60; Indels 13; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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FIBROIN HEAVY CHAIN.
HIGHLY REPETITIVE.
INTERCHAIN (WITH LIGHT CHAIN).
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; 8EE11D3A0A47440E CRC64;
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Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases
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modified and this statement is not removed.
              entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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                                                                     EMBL; V00094; CAA23432.1; --
EMBL; V00097; CAA23433.1; --
EMBL; X34439. AAB31861.1; --
EMBL; X13669; CAA32076.1; --
EMBL; M35378; AAA27893.1; --
EMBL; AB017362; BAA33147.1; --
SILK; S01844; S01844.
SILK; S1gnal; Repeat.
                                                          EMBL; AF226688; AAF76983.1; -.
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DISULFID
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YS89_CAEEL
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1156 SGTTASGSGSSGGSSG-TGSDGVNSGKTTALNGDGTGSGTATTPGSHLGDGGSTSGSGD- 1213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        353 STITYIVGAGVEAVTVSVSATSNGTESGGAGS--GTGTSVSATSTLTGNGGTESGGTAG- 409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  344726 MW; F8239436D03666CD CRC64;
                                                                                                                                                                                                                         SER/THR-RICH.
GLY/SER-RICH.
                                              InterPro; IPR002111; Cat_channel_TrpL.
InterPro; IPR001024; Lipoxygenase_LH2.
InterPro; IPR0010636; Marchannel_nlg.
InterPro; IPR000203; PKD_cys_rich.
Pfam; PF01825; Ion_trans; 1.
Pfam; PF01825; GPS; 1.
SWART; SM00303; GPS; 1.
SWART; SM00308; LH2; 1.
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                                                                                                                                                                                                       Transmembrane.
        EMBL, Z48544; CAB70201.1; JOINED. WormPep; ZK945.9; CE25697.
EMBL; Z48582; CAB70201.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 7.0 Best Local Similarity 34.9 Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3178 AA;
                                                                                                                                                                                                         Hypothetical protei
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2483
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Search completed: July 16, 2003, 17:47:30 Job time: 31.688 secs

454 AGTGTSGTTTSSGTGAGGAGSGGPSG 479

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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Fibroin heavy chain precursor (Fib-H) (H-fibroin).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360 GAGVEAVIVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAG 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   420 GTSGTTTSSGAASGKAG-TGTAGTT----TSSEGAGSDKAGTGTSGTTTSSG----- 466
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STRAIN-CDC 1551 / Oshkosh;
Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
Pleischmann R.D., Alband D., Eisen J.A., Earnolaeve E., Hickey E.,
Rolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,
                                                               ۵,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23; Gaps
                                                                                                                                                                                                                                                                                               "Whole genome comparison of Mycobacterium tuberculosis clinical and
                                           MEDLINE=9829597; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Cole S.T., Brosch R., Parkhill J., Gas S., Bary C.E. III, Tekala F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Shurnsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Seeger K., Skelton S., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J. E., Taylor K., Whitehead S., Barrell B.G.; Bociphering the biology of Mycobacterium tuberculosis from the Complete genome sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7.2%; Score 183.5; DB 1; Length 778;
                                                                                                                                                                                                                                                                                                         laboratory strains.";
Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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Q -> H (IN REF. 2).
A -> T (IN REF. 2).
; DABZOFE58E4999E7 CRC64;
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EMBL; AE007103; AAK47026.1; ALT_INIT.
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TubercuList; Rv2634c; -.
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63 · 65
· 274
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CONFLICT 51 51
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                         SEQUENCE FROM N.A.
 NCBI_TaxID=1773;
                                                                                                                                                                                                                                                                                                                                                 SUBFAMILY
                                                                                                                                                                                                                                                                                    Bishai W.;
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Matches (
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5263 AA.

PRT;

FBOH_BOMMO STANDARD; P05790; Q26379; Q17220; O1-NOV-1988 (Rel. 09, Created)

FBOH_BOMMO RESULT 14

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BUTALINE-99296390; PubMed-10366732;

Tanaka K., Kajiyama N., Ishikura K., Waga S., Kikuchi A., Ohtomo K.,

Takagi T., Mizuno S.;

Biochim Biophys Acta 143:92-103(1999).

INCOLUBLE AND THE SILK FILMANT: A STRONG, INEXTENSIBLE,

INSOLUBLE AND CHEMICALLY INERF. FIRE.

A DISULFIDE BOND. HEAVY LIGHT CHAIN ASSEMBLY IS ESSENTIAL FOR THE FEPTICENT INTRACELLULAR TRANSPORT AND SECRETION OF FIBROIN.

INCOLUBLE SPECIFICITY: PROUCED EXCLUSIVELX IN THE POSTERIOR (PSG)

SECTION OF SILK GLANDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SILK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Highly repetitive structure and its organization of the silk fibroin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tsujimoto Y., Suzuki Y.; "The DNA sequence of Bombyx mori fibroin gene including the 5' flanking, mRNA coding, entire intervening and fibroin protein coding
                         Domaryota; Morra Morring Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombycoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mita K., Ichimura S., Zama M., James T.C.; "Specific codon usage pattern and its implications on the secondary structure of silk fibroin mRNA.";
                                                                                                                                                                                                                                                                 MEDILINE-20330362; PubMed-10871375;
Zhou C.-z., Confalonieri F., Medina N., Zivanovic Y., Esnault C.
Yang T., Jacquet M., Janin J., Duguet M., Perasso R., Li Z.-G.;
"Fine organization of Bombyx mori fibroin heavy chain gene.";
Nucleic Acids Res. 28:2413-2419(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PARTIAL SEQUENCE FROM N.A. MEDLINE-79211211; Pubmed-455439; Suzulimoto Y., Suzuki Y.; "Structural analysis of the fibroin gene at the 5' end and surrounding regions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 5179-5263 FROM N.A., AND DISULFIDE BONDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-168 FROM N.A. MEDLINE-80045039; PubMed-498286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Biol. 203:917-925(1988).
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Bombyx.mori (Silk moth)
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Cell 16:425-436(1979)
                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                NCBI_TaxID=7091;
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SUBFAMILY,
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P71933;
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                           ISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTES
                                                                                        IFSKKLLVSFGSLVALASIPLIAISCGQT-NTDKSQQPGSGSSTSGGQSGTGLGS-GTTT
                                                                                                                                                             GGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGT-TT
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Li-Weber M., de Groot E.J., Schweiger H.G.;

"Sequence homology to the Drosophila per locus in higher plant nuclear DNA and in Acetabularia chloroplast DNA.";

Mol. Gen. Genet. 2093:1-7(1987).

-1- SIMILARITY: TO THE PERIOD CLOCK PROTEINS OF DROSOPHILA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S00273; S00273.
Biological rhythms; Repeat; Chloroplast.

DOMAIN 49 138 45 X 2 AA TANDEM REPEATS OF G-T.
SEQUENCE 174 AA; 16878 MW; E6C06770E9DDCB5D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Period clock protein (P230).
Acetabularia mediterranea (Mermaid's wine glass).
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40.3%; Pred. No. 0.00075;
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                                                                                                                                                                                                                                                                                           SSGTGAGGAGS----GGPSGHASNAKIPG 488
                                                                                                                                                                                                                                                                                                                                                      117 SQDSGAKGTGSDSQDSGAKGTGSDSQDSG
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16-OCT-2001 (Rel. 40, Last seq
15-JUN-2002 (Rel. 41, Last ann
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Dasycladaceae; Acetabularia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PER_ACEME
P12347;
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                                                                                                                                                                                                                                                                                               464
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YZ08_MYCTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PER_ACEME
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               573 GADNPTGIGGTGGTGGKGGAGGAGGQGGSSGAGGTNGSGGAG----GTGGQGGAGGAGGA 628
                                                                                                                                                                                                                                                                                                                                                                                                                               Harris D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          411 TTSSGTEAGGTSGTTTSSGA--ASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          360 GAGVEAVIVSVSATSNGTE-SGGA----GSGTGTSVSATSTLTGNGGT----ESGGTAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            513 GAGSAGTDATATGATGGTGFSGGAGGAGGAGGNTGVGGTNGSGGQGGTGGAGGAGGAGG
                                                                                                                                                           Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Actinobacteria; Actinobacteria (class); Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriae
                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-9892987; PubMed=9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeler K., Gas S., Bary C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krooph A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL PE-PGRS FAMILY PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nature 393:537-544(1998).
-!- SIMILARITY: BELONGS TO THE MYCOBACTERIAL PE FAMILY. PGRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.2%; Score 185; DB 1; Length 1901; 37.8%; Pred. No. 0.02; Live 12; Mismatches 55; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1901 AA; 147627 MW; C7B1923D5D0146CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Repeat; Signal; Complete proteome.
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PE-FGRS family protein Rv3508 precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical PE-PGRS family protein Rv2634c.
Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             778 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ----TGAGGAGSGGPSGHASNA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   629 GADNPTGIGGAGGTGGTGGAAGA 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RV3508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ProDom; PD001223; PE_region; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TubercuList; Rv3508; -. InterPro; IPR000084; PE_region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL022022; CAA17745.1; -.
                                                                                                                        Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypothetical protein; R SIGNAL 1 30
                                                                                 RV3508 OR MTV023.15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00934; PE;
                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     NCBI_TaxID=1773;
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                                                                                                                               281 KAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKI 340
                                                                                 -----GEGSSSGGGGRRG-----GS 467
                                                        341 N-RDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGN 399
                                                                                                                GGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTS 459
                         388 ASLAETEGRYCVQLSQIQSQISALEEQLQQIRAETECQNAEYQQLLD------IKT 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Probable).
MISCELLANEOUS: THE NUMBERS OF REPEATS CAN VARY AND IS ONE OF THE
BASIS OF THE ANTIGENIC DIVERSITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADAPTATION. -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-92097525; PubMed=1721868;
Yogev D., Rosengarten R., Watson-Mckown R., Wise K.S.;
"Molecular basis of Mycoplasma surface antigenic variation: a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            set of divergent genes undergo spontaneous mutation of periodic coding regions and 5' regulatory sequences."; EMBO J. 10:4066-4079(1991).
-- FUNCTION: RESPONSIBLE FOR THE ANTIGENIC DIVERSITY FOR HOST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13;
                                                                                                                                                                                                                                                                                                                                                                                            Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-ACYL DIGLYCERIDE (PROBABLE).
7 X 12 AA TANDEM REPEATS.
                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
1-DEC-1992 (Rel. 24, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Variant surface antigen B precursor (VLPB prolipoprotein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT SURFACE ANTIGEN B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28F4C9ECA85585D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lipoprotein; Repeat; Signal.
29 PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; Score 190.5; DB 1
35.6%; Pred. No. 0.00058;
ive 25; Mismatches 58
                                                                                                                                                                                                                                                                            174 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; S18654; S18654.
PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
                                                                                                                                                                         GTTTSSGTGAGGAGSGGPSGHASNA 484
                                                                                                                                                                                                     521 GGSSSGGAGGHGGSSGGGYGGSSS 545
                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; X62936; CAA44709.1; ALT_SEQ.
                                                                        : | :|: ||
438 RLENEIQTYRSLLE------
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                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                Mycoplasma hyorhinis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antigen; Membrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    174 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best_Local Similarity
Matches 53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=2100;
                                                                                                                                                                                                                                                                            VLPB_MYCHR
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                                                                                                                 400
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REPEAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KELTTEIDSNIEDMSSH-----KSEITELRRTVQGLE-----IELQSQLALKQSLE 387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EQFIKNELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYE---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QFKS------VVTTPADVAGV------SDGFFIRGQNLGAVGSVNEQPNTVGMSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 YYKTIEDLKGQILTLTTDNANVLLQIDNARLAADDFRLKYEN------EVTLRQSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------EFIEKLRGARSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 VNVEMNAAPGVDLTQLLNNMRNQ----YEQLAEKNRKDAEEWFNQKS------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSLLA-SGEVTS---NFR---YISKEYEYEHTELAKEHCKKEKCVNVDNIEDNNLKIYAK
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OSVLEL (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7.5%; Score 192; DB 1; Length 569;
22.0%; Pred. No. 0.002;
tive 68; Mismatches 192; Indels 134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                MISSING (IN REF. 2).

SY -> GC (IN REF. 2).

S -> G (IN REF. 2).

Q -> R (IN REF. 2).

WYEKHGNSGO -> VVREARQLKP (IN RESEDEM -> OSYLEL (IN REF. 2).

E -> A (IN REF. 2).

EGRYCV -> VESLLR (IN REF. 2).

EGRYCY -> VESLLR (IN REF. 2).

EGRYCS -> OGGRGGG (IN REF. 2).

GGSHGGGS -> CGGRGGG (IN REF. 2).

H -> R (IN REF. 2).

H -> R (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S -> G (IN REF. 2).

S -> G (IN REF. 2).

GQ -> RR (IN REF. 2).

KS -> SGT (IN REF. 2).

4). EEC59D4D8FFE484D CRC64;
                                                                                                                                                                                                                                                                                                                                                               S -> C (IN REF. 2).
S -> F (IN REF. 2).
S -> F (IN REF. 2).
Y -> L (IN REF. 2).
E -> G (IN REF. 2).
AG -> GS (IN REF. 2).
                                                                                                                                                         PRINTS; PR01248; TYPEIKERATIN.
PROSITE; PS00226; IF; 1.
Intermedlate filament; Colled coil; Keratin.
                                                                                                                                                                                                                                                                                                                                                     GLY/SER-RICH.
email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       LINKER 12.
                                                                                                                                                                                                                                                              COIL 1A.
LINKER 1.
                                                                                                                                                                                                                                                                                           COIL 1B.
                                                                                                                                                                                                                                                                                                                                  STUTTER.
                           EMBL; L00193; AAA39391.1; -. EMBL; M10081; AAA39391.1; JOINED. EMBL; V00830; CAA24214.1; -.
                                                                  PIR: A02940; KRWSE1.
PIR: S07330; S07330.
MGD; MGI:96685; Krt1-10.
InterPro; IPR001664; IF.
InterPro; IPR002957; Keratin_I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57711 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      569 AA;
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                                                                                                                                           Pfam; PF00038;
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(See http://www.isb-sib.ch/announce/
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                                                                                                                                                          7.5%; Score 193.5; DB 28.7%; Pred. No. 0.0013;
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   modified and this statement is not removed.
                                                                                                                                                                                40; Mismatches
                                                                                                                           GLY/SER-RICH
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             entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                          POLY-SER.
                                                                                                     POLY-ARG.
                                                                                                                THR-RICH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                    45873 MW;
                                             EMBL; AJ133745; CAB39735.1;
                                                                                                                                                                                51; Conservative
                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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450
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82
339
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79
303
355
450 AA;
                                                           Sporulation; Signal
                                                                                                                                                                       Similarity
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SEQUENCE
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                                                                                                                                   IYHTISSQ----ISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGARSEGN 185
                                                                                                                                                        439 TYETVMKKGOTAGASFCSKPYRFLIQNGCYVL-LETEWTSFVNPWSRKLEFVVG----HH 493
                                                                                                                                                                                                                                       SGASGPMSP-VHEGSGGSGSSGNETTASNIHMSSVTNTSIAGTG-----GTGTGTGTG 705
                                                                                                                                                                                                                                                                                                                                                                           428
                                                                                                                                                                                                                                                                                           PHHDYYDSKSST - - - ETPPSYNQLNYNENLLRFFNSKPVTAPAELDPPKTEPPEPRGTCV 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GEVTSNFRYISKEYEHTEL----AKEHCKKEKCVNVDNIEDNNLKIYAKQFKSVVT
                                                          TPADV-AGVSDGFFIRGONLGAVGSVNE------QPNTVGMSLEQFIKNELYSFSNE
                                                                                                       NMFQ------EALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDG
                                                                                                                                                                                            NTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTE
                                                                                                                                                                                                                         238 YDFDYINTKKELV----ILASVLDGL-----DLIMERLIENFSDVNNTDDIKKA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---------GAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bohne W., Ferguson D.J.P., Kohler K., Gross U.;
"Molecular characterisation of a developmentally expressed spore wall
protein from the human microsporidian Encephalitozoon cuniculi.";
Submitted (MAR-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                              SG-GAGSGTGTSV-SATSTLTGNG-GTESGGTAGTTTSSGTEAGGTSGTTTSS-----
                                                                                                                                                                                                                                                                                                                                                                                                                             766 PPVTLTESLLNKHNDEMEKFMLKKHRESRGRTGEKSKKSANDTLKMLEYSGPGHGIKRGG
 Length 1224;
                        Indels
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Eukaryota, Microsporidia, Unlkaryonidae, Encephalitozoon.
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  DB 1;
                       220;
7.7%; Score 196.5; DB 21.7%; Pred. No. 0.0029; iive 69; Mismatches 22
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(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
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                       Conservative
          Similarity
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30-MAY-2000
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                      136;
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Q9XZV1;
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  Query Match
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modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                             315 VTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATS 374
                                                                                                                                                                                                               287 ITAITNALQANKNNFVTFFTTQTTNLQTDVQNALTALITALTTLTS-----TTSTEFTQ 340
                                                                                                                                                                                                                                                                    375 -----NGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGGTSGTT 425
                                                                                                                                                                                                                                                                                                                                                                                                         426 TSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGHASN 483
                                                                                                                                                                                                                                                                                                   p02535; p08731;
21-070-1986 (Rel. 0), Created)
01-AUG-1988 (Rel. 08, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Keratin, type I cytoskeletal 10 (Cytokeratin 10) (56 kDa cytokeratin)
(Keratin, type I cytoskeletal 59 kDa).
                                                                                                            Gaps
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Sciurognathi; Muridae; Murinae; Mus
                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-85207552; PubMed-2581944; Krieg T.M., Schafer M.P., Cheng C.K., Filpula D., Flaherty P., Steinert P.M., Roop D.R.; Organization of a type I keratin gene. Evidence for evolution
                                                 DB 1; Length 450;
                                                                                                      Indels
5E7071A3E3A6DF60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   intermediate filaments from a common ancestral gene.";
J. Biol. Chem. 260:5867-5870(1985).
                                                                                                   64;
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STRAIN-Oregon-R;
MEDLINE-86545055; PubMed-3087625;
REddy P., Jacquier A.C., Abovich N., Petersen G., Rosbash M.;
Reddy P., Jacquier A.C., Abovich N., Petersen G., Rosbash M.;
The period clock locus of D. melanogaster codes for a proteoglycan.";
Cell 46:53-61(1986).
                                                                                       "DNA sequence variation at the period locus within and among species of the Drosophila melanogaster complex."; Genetics 133:375-387(1993).
                   SEQUENCE OF 499-1075 FROM N.A. (ISOFORM PER-A)
                                                                   SEQUENCE OF 63-573 FROM N.A. (ISOFORM PER-A). MEDLINE-93170641; PubMed-8436278; Kliman R.M., Hey J.;
      Science 287:2220-2222(2000).
                                                                                                                    PHOSPHORYLATION.
 melanoqaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                        BEHAVIOR.
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PHOSPHORYLATION
RAPELINE=94181572; Pubmed=8134384;
RA MEDLINE=94181572; Pubmed=8134384;
RT MEDLINE=94181572; Pubmed=8134384;
RT Temporal phosphorylation of the Drosophilal period protein.";
Proc. Natl. Acad. Sci. U.S.A. 91:2260-2264(1994).
LT-COC. Natl. Acad. Sci. U.S.A. 91:2260-2264(1994).
RHYTHAIC COMPONENT OF THE MALE COURTSHIP SONG THAT CREADIAN RHYTHAIC COMPONENT OF THE MALE COURTSHIP SONG THAT ORIGINARES IN THE THORACIC NERVOUS SYSTEM. THE BIOLOGICAL CYCLE DEBENDS ON THE RHYTHAIC COMPONENT OF THE MALE COURTSHIP SONG THAT TORICINARES IN THE THORACIC SYSTEM. THE BIOLOGICAL CYCLE DEBENDS ON THE RHYTHAIC COMPONENT OF THE MALE COURTSHIP SONG THAT THE TICHALD ON THE TIMA-PER COMPLEX. LIGHT INDUCES THE DEGRADATION OF TIM WHICH PROMOTES ELIMINATION OF PER. NUCLEAR ACTIVITY OF THE HETRODIMER COORDINATIVE RESULATES PER AND TIM TRANSCRIPTION THROUGH A NUCLEAR ACTIVITY OF THE HETRODIMER OF TRANSCRIPTIONAL LOOP. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN SUGGESTING TRANSCRIPTIONAL INHIBITION.
CC. TRANSCRIPTIONAL INHIBITION.
CC. TRANSCRIPTIONAL INHIBITION.
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CC. EXPRESSION OSCILLATES IN ALL TISSUES STUDIED EXCEPT FOR THE OVARY.
CC. EXPRESSION OSCILLATES IN ALL TISSUES STUDIED EXCEPT FOR THE OVARY.
CC. LIGHT.

DOMAIN: CONTAINS A REMARKABLE RUN OF ALTERNATING GLY-THR RESIDUES WHICH IS POLYMORPHIC IN LENGTH. AT LEAST THREE TYPES OF GLY-THR LENGTH EXIST IN THE NATURAL POPULATION, (GLY-THR)23 (SHOWN HERE), AND TWO MAJOR VARRANTS (GLY-THR)17 AND (GLY-THR)20. THIS GLY-THR STRETCH IS IMPLICATED IN THE MAINTENANCE OF CIRCADIAN PERIOD AT BIFFERRY TEMPERATURES. DELETION OF THE REPEAT LEADS TO A SHORTENING OF THE COURTSHIP SONG CYCLE PERIOD, AND THUS COLLD BE IMPORTANT FOR DETERMINING FEATURES OF SPECIFIC MAING

DOMAIN: MUTATIONS IN THE PAS DOMAIN RESULT IN LONGER CIRCADIAN RHYTHMS AND COURGEHIP SONG (PERL MUTATION) OR MAKES THE FLIES ARRHYTHMIC (PEROI MUTATION).

PTM: PHOSPHORYLATED WITH A CIRCADIAN RHYTHMICITY, PROBABLY BY THE DOUBLE-TIME PROTEIN (DBT). PHOSPHORYLATION COULD BE IMPLICATED IN THE STRALLITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER PER-TIM. -

SIMILARITY: TO OTHER G-T STRETCH CONTAINING PROTEINS.
SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
DATABASE: NAME-PROTEIN Spotlight;
NOTE-ISSUE 6 of January 2001; + + + +

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56 79 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
57 297 PAS 1.
77 447 PAS 2. REGULATES THE RHYTHM OF SPECIES-SPECIFIC MISSING (IN ISOFORM PER-A/SHORT). MISSING (IN ISOFORM PER-B). MISSING (IN ISOFORM PER-D AND ISOFORM WWW="http://www.expasy.org/spotlight/articles/spt1t006.html". Nuclear protein; Phosphorylation; G -> V (IN REF. 6; AAA28777). GP -> A (IN REF. 6; AAA28777). E -> A (IN REF. 5). T -> S (IN REF. 1 AND 4). TAA -> RR (IN REF. 3 AND 5). MISSING (IN (GLY-THR)20). MISSING (IN (GLY-THR)17). W (IN ISOFORM PER-E) REPEATS COURTSHIP POLY-GLU. POLY-ALA. POLY-GLY. POLY-GLY. POLY-ALA POLY - ALA POLY - ALA POLY-LYS InterPro; IPR001610; PAC. InterPro; IPR000014; PAS_domain. Pfam; PF00989; PAS; 2. X03636; CAA27285.1; -. AL024485; CAA19677.1; -. AL024485; CAA19678.1; -. AL024485; CAA198699.1; -. D00009; BAA00007.1; -. EMBL; M30114; AAA28752.1; -. M30114; AAA28754.1; -. AF033029; AAB87476.1; M30114; AAA28753.1; -. PROSITE; PS50112; PAS; 2. Biological rhythms; Repeat; L07825; AAA28769.1; -AAA28777.1; -AAA28776.1; -AAA28775.1; -AAA28773.1; -L07823; AAA28771.1; -FlyBase; FBgn0003068; per 879 905 914 1013 1041 868 702 708 211 499 637 762 62 963 958 1224 SMART; SM00086; PAC; 1 SMART; SM00091; PAS; 2 PIR; A23932; UMFF 697 697 2111 498 637 762 L07819; L07821; L07818; Polymorphism; L07817 VARIANT CONFLICT CONFLICT CONFLICT CONFLICT VARSPLIC VARSPLIC VARSPLIC /ARSPLIC VARIANT DOMAIN DOMAIN DOMAIN DOMAIN EMBL;

141 141 141 AA; 12325 MW; E407A197912E3AE2 CRC64;

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-1- SUBUNIT: FORMS HETERODIME WITH TIMELESS (TIM); THE COMPLEX THEN TRANSCRIPTIONAL INHIBITION (BY SIMILARITY).

-1- SUBCELLULAR LOCATION: NUCLEAR AT SPECIFIC PERIODS OF THE DAY. FIRST ACCUMILARES IN THE DEFINIOLAR REGION ABOUT ONE HOUR BEFORE TRANSCRIPTION INTO THE NUCLEAR REGION MITH TIM IS REQUIRED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
518 SMSGSSSRGGGSGGGR-----YGGGGSYGGG-----SGGGSYGGSSGGGSGGSYG 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FOR NUCLEAR LOCALIZATION (BY SIMILARITY).

DOMAIN: THE RUN OF GLY-THR IS IMPLICATED IN THE MAINTENANCE OF CIRCADIAN PERIOD AT DIFFERENT TEMPERATURES. DELETION OF THE REPEAT LEADS TO A SHORTENING OF THE COURTSHIP SONG CYCLE PERIOD, AND THUS COULD BE IMPORTANT FOR DETERMINING FEATURES OF SPECIES-SPECIFIC MATING BEHAVIOR (BY SIMILARITY).

PHER PHOSPHORYLAND MITH A CIRCADIAN RHYTHMICITY, PROBABLY BY THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: ESSENTIAL FOR BIOLOGICAL CLOCK FUNCTIONS. DETERMINES THE
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                                                                                                                                                                                                                                                                    Drosophila serrata (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=93196482; PubMed=8450754;
Peixoto A.A., Campesan S., Costa R.H., Kyriacou C.P.;
"Molecular evolution of a repetitive region within the per gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rhythms; Repeat; Nuclear protein; Phosphorylation.
                                 433 GKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGG 476
                                                     564 GGSGGGSSGGRRGGSGGGGSSGGSYGG---SSGGGRGGSSSGG 604
                                                                                                                                                                                  01-0CT-1993 (Rel. 27, Created)
01-0CT-1993 (Rel. 27, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
                                                                                                                                                        141 AA
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POLY-SER.
                                                                                                                                                                                                                                         Period circadian protein (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Evol. 10:127-139(1993)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      flyBase; FBgn0012804; Dser\per.
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121
128
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Mol. Biol.
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NON_TER
                                                                                                                                                        PER_DROSR
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8
                                                                                                                                       369 SVSATSNGTESGGAGSGTGTSVSATSTLTGNG-GTESGGTAGTTTSSGTEAGGTSGTTTS 427
                                                                                                                                                                                 "A family of unusually spliced biologically active transcripts encoded by a Drosophila clock gene.";
Nature 326:42-47(1987).
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Baylies M.K., Weiner L., Vosshall L.B., Saez L., Young M.W.; "Genetic, molecular and cellular studies of the period locus and its products in Drosophila melanogaster.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-87144607; PubMed-3102970;
Citri Y., Colot H.V., Jacquier A.C., Yu Q., Hall J.C., Baltimore D.,
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                                                                                                                                                                                                                                                                              428 SGAASGKA-GTGTA-GTTTSSEGAGSDK-AGTGT-SGTTTSSGTGAGGAGSGGP 477
                                                                                                                                                                                                                                                                                                                 PER_DROME STANDARD; PRT; 1224 AA.
P07663; 017483; Q24446; Q24447; Q24448; Q24449; O76882; O76883; O76884; O76885;
O1-APR-1988 (Rel. 07, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                   6
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Length 141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. (ISOFORMS PER-A/LONG; PER-B AND PER-C).
                                                                       Indels
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Jackson F.R., Bargiello T.A., Yun S.-H., Young M.W.;
"Product of per locus of Drosophila shares homology with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Period circadian protein (Clock-6 protein) (CLK-6).
Score 199.5; DB 1
Pred. No. 0.00015;
                                                                   16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM PER-A/SHORT).
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   7.8%;
                            Similarity 49.18;
                                                                   56; Conservative
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Nature 320:185-188(1986).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-Oregon-R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New York (1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Oregon-R;
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   Query Match
Best Local 3
                                                                       Matches
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L C G G C C C C C C C C C C C C C C C C	M10937, AADO1911.1; 02951; KRMS2. 2DPAGE; P04104; MOUSE. GI:96698; Krt2-1. ro; IPR001664; IF. FF00038; filament; 1. ediate filament; Colled ET 1 186 187 496	DOMAIN 497 627 TAIL DOMAIN 187 222 COIL DOMAIN 223 242 LINKER I DOMAIN 243 333 COIL 1B. DOMAIN 334 357 LINKER I2. DOMAIN 358 496 COIL 2. SITE 451 STUTTER. SEQUENCE 627 AA; 65092 MW; EF7E8486545395	DEST LOCAL Similarity 21.34; Pred. No. 0.00076; Matches 99; Conservative 61; Mismatches 134; Indels 170; Gaps 17; Qy 150 VKHDNYILKKEGEGCEQIYNYEEFIEKLR	0y 245 TKKELVILASVLDGL
 Similarity 22.6%; Pred. No. 0.00029; 9; Conservative 74; Mismatches 162; Indel GVSDGFFIRGQNLGAVGSVNEQPNIVGMSLEQFIRNELYSFE	184 KSLNNQFASFICKVRFLEQQNQVLQTKWELLQQVDTSTRTHNLEPFESFINNLRRRVDQ 179GARSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNF	SCKS-NAIILKKKILDNDEDYKINFREMVNE SVKAQNEDIAQKSKABAESLYQSKYEEL	Db 452 QAKEDLARLLRDYGELMITKLALDLETATYRTLLEGEESRMSGECAPNYSYSYSTSHTTI 511 Qy 374 SNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGT-TTSSGTAGGTSGTTTSGGAAS 432 Db 512 SGGGRGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	RESULT 5 K2C1_MOUSE ID K2C1_MOUSE STANDARD; PRT; 627 AA. AC P04104. DT 01-NOV-1986 (Rel. 03, Created) DT 30-NAY-2000 (Rel. 39, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last sequence update) DT 16-OCT-2001 (Rel. 40, Last annotation update) DT 16-OCT-2001 (Rel. 40, Last annotation update) DT MART OR KRT2-1. GN KRT1 OR KRT2-1. OS Mus musculus (Mouse). OC EUKARYOCA: Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi; OC EUKARYOCA: Metazoa: Chordata; Sciurognathi; Muridae; Murinae; Mus. OC EUKARYOCA: Money 1. SEQUENCE OF 83-628 FROM N.A. RN 11

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MEDLINE-93107743; PubMed-1281859;
    BEQUENCE FROM N.A.
Hatsell S.J., Eady R.A., Wennerstrand L., Dopping-Hepenstal P.,
Leigh I.M., Munro C., Kelsell D.P.;
"Novel splice site mutation in keratin 1 underlies mild epidermolytic
palmoplantar keratoderma in three kindreds."
Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
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               01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last amnotation update)
16-TUN-2001 (Rel. 1) (Stockeletal 1 (Cytokeratin 1) (Kl) (CK 1) (67 kDa cytokeratin) (Hair alpha protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                        "Amino acid sequences of mouse and human epidermal type II keratins of Mr 67,000 provide a systematic basis for the structural and functional diversity of the end domains of keratin intermediate filament subunits.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARIANTS EHK GLY-154; SER-187 AND PRO-192.
MEDLINE-94117869; PubMed-7507151;
Yang J.-M., Chipev C.C., Digiovanna J.J., Bale S.J., Marekov L.N.,
Steinert P.M., Compton J.G.;
"Mutations in the H1 and IA domains in the keratin I gene in
epidermolytic hyperkeratosis.";
                                                                  KRT1 OR KRTA.
Homo saptens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chipev C.C., Korge B.P., Markova N., Bale S.J., Digiovanna J.J., Compton J.G., Steinert P.M.;
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Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
Morley S.M.;
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                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-85166239; PubMed=2580302;
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"Structure of a gene for the human epidermal 67-kDa keratin."
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MEDLINE-85207740; PubMed=2581964;
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VARIANTS EHK PRO-185 AND SER-187.
MEDLINE=94117870; PubMed=7507152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=92386601; PubMed=1381288;
20-MAR-1987 (Rel. 04, Created)
01-FEB-1996 (Rel. 33, Last seq
15-JUN-2002 (Rel. 41, Last ann
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                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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VARIANT ALLELE 1B.
                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hyperkeratosis
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                                                                                                                                                               PORESKIN. THE 67-KDA TYPE II KERATINS ARE EXPRESSED IN TERMINALLY DIFFERENTATING EPIDERMIS.

POLYMORPHISM: THERE ARE TWO SIZE VARIANTS OF KRT1, TERMED IA AND 1B WITH ALLELIC FREQUENCIES OF 0.61 AND 0.39. 1B LACKS 7 LACKS 7 RESIDUES COMPARED TO 1A.

DISEASE: DEPECTS IN KRT1 ARE A CAUSE OF EPIDERMOLYTIC HYPERKERATOSIS (EHK) (ALSO KNOWN AS BULLOUS CONGENITAL CHTHVOSIFORM EXYTHRODERMA (BIE)); A HEREDITARY SKIN DISORDER CHARACTERIZED BY BLISTERING AND A MARKED THICKENING OF THE STRATUM
                        to a deletion in the
Korge B.P., Compton J.G., Steinert P.M., Mischke D.;
The two size alleles of human keratin I are due to a deletion in t
glycine-rich carboxyl-terminal V2 subdomain.";
J. Invest. Dermatol. 99:697-702(1992).
-!- SUBUNIT: HETEROFETRAMER OF TWO TYPE I MOD TYPE II KERATINS.
KERATIN I IS GENERALLY ASSOCIATED WITH KERATIN 10.
-!- TISSUE SPECIFICITY: THE SOURCE OF THIS PROTEIN IS NEONATAL
                                                                                                                                                                                                                                                                                                                                                                                                   MISCELLANEOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBELLIAR KERATIN: I (ACIDIC; 40-55 kDa) [K9 TO K20] AND (NEUTRAL TO BASIC; 55-70 kDa) [K1 TO K8].
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT.FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01276; TYPE2KERATIN.
PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation;
Polymorphism; Phosphorylation.
INT_MET 0 0 BY SIMILARITY.
DOMAIN 1 178 HEAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLY/SER-RICH.
PHOSPHORYLATION (BY SIMILARITY).
V -> G (IN EHK).
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L -> P (IN EHK).
/FTId=VAR_003854.
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N -> S (IN EHK).
/FTId=VAR_003856.
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LINKER 1.
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EMBL; M98776; AAB47721.1; --
EMBL; AF304164; AAG41947.1; --
EMBL; M10938; AAA36153.1; ALT_SEQ.
PIR; A02950; KRHUZ.
PIR; A22940; AZ2940; AZ29406; NEPHGE.
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InterPro; IPR003054; Keratin_II.
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MIM; 113800;
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P04264; Q14720; Q9H298;
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   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Burpaen Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                          MEDINE-9503883; PubMed-7524919;
Rothnagel J.A., Traupe H., Wojcik S., Huber M., Hohl D.,
Pittelkow M.R., Saeki H., Ishibashi Y., Roop D.R.;
"Mutations in the rod domain of keratin 2e in patients with ichthyosis
bullosa of Siemens.";
                                                                                                                                                                                                                                              MEDLINE-99181809; PubMed-10084318; Arin M.J., Longley M.A., Epstein E.H. Jr., Scott G., Goldsmith L.A., Rothmagel J.A., Roop D.R.; "A novel mutation in the 1A domain of keratin 2e in ichthyosis bullosa of Siemens.";
                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97348962; PubMed-9204966;
Yang J.-M., Lee S., Bang H.-D., Kim W.-S., Lee E.-S., Steinert P.M.;
"A novel threonine-to-proline mutation at the end of 2B rod domain in the Keratin 2e chain in ichthyosis bullosa of Siemens.";
J. Invest. Dermatol. 109:116-118(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- DISEASE: DEFECTS IN KRT2A ARE A CAUSE OF ICHTHYOSIS BULLOSA OF SIEMENS (IBS), A RARE AUTOSOMAL DOMINANT DISORDER DISPLAYING A TYPE OF PRIDENDLYTIC HYPERKERATOSIS CHARACTERIZED BY EXTENSIVE BLISTERRING FROM BIRTH. HYPERKERATOSES AND SHEDDING OF THE OUTER LAYERS OF THE EPIDERMIS (MOLTING) ARE OBSERVED IN LATER WEEKS.
-!- MISCELLANHOUS: THERE ARE TWO TYPES OF CYTOSKELETAL AND MICROFIBALLAR KERATIN: I (ACIDIC; 40-55 kDa) [K9 TO K20] AND II (NEUTRAL TO BASIC; 56-70 kDa) [K1 TO K8].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- DEVELOPMENTAL STAGE: SYNTHESIZED DURING MATURATION OF EPIDERMAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation;
                                                                                                                                                                                                                                                                                                                        J. Invest. Dermatol. 112:380-382(1999).
[8]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAIL.
COIL 1A.
LINKER 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ROD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR003054; Keratin_II.
[5]
VARIANTS IBS ASP-493 AND LYS-493
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01276; TYPE2KERATIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METAPLASIAS AND CARCINOMAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF019084; AAB81946.1; -. PIR; A44861.
                                                                                                   Genet. 7:485-490(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M99061; AAC83410.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00038; filament;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:6439; KRT2A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001664; IF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              183
493
645
219
238
                                                                                                                                VARIANT IBS PRO-485.
                                                                                                                                                                                                                                    VARIANT IBS ASN-188.
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494
184
220
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MIM; 146800;
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                                                                                                   Nat.
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COIL 1B. LINKER 12. COSIL 2. PHOSPHORYLATION (BY SIMILARITY). O -> P (IN IBS). ATIC-VAR_OOSS65. I -> N (IN IBS). ATIC-VAR_OOS165. N -> D (IN IBS). ATIC-VAR_OOSS165. N -> Y (IN IBS). ATIC-VAR_OOSS165. T -> F (IN IBS). ATIC-VAR_OOSS185. T -> P (IN IBS). ATIC-VAR_OOSS186. T -> P (IN IBS). ATIC-VAR_OOSS186. T -> P (IN IBS). ATIC-VAR_OOSS186. AMM; EBOZSAL73833499A CRC64;	# 5.5%; Score 217; DB 1; Length 645; conservative 100; Mismatches 200; Indels 122; Gaps 26; GIHYYXIDGSLLASGEVTSNERYEYEYEHTELAKEHCKKEKCVNVDNI 61	rny LCNQ LSA EAE EAE FSD	VQDATADAEGRGEHALKDARNRINDLEEALQQAREDL 40 ISSYKLLLSTITYIVGAGVEAVTVSVSA 37 :: : : : IATYRKLEGEECRMSGDLSSNYTVSYTSSTISSNYASKA 52 TSTLTGNGGTESGGTAGTTSSGTEAGGTSGTTTSSGAAS 43 :: : : : : GSSYGSGGROSGSRG-SGGGSISGGTGSGGGGRY 57 DKAGTGTGTGTGAGGASSISGGSGGRY 57 DKAGTGTSGTTTSSGTGAGGASSGPSGHASNA 48 :: GGKHSSGGGSRGGSSSGGGSGGSSSVKGSSGEAFGS 63	PRT; 643 AA.
330 354 493 662 187 192 192 485 490 493 493	larity 22.1%, Conservative 1 YYYIDGSLLASGEVI :: EVSVNQSLL NLKIYAKOFKS	KKAPECKS LYDAELSCI EDYKKYED EDYKKYED LYDAELSCI LYDAELSCI EDDELFKKA EDDELFKKA KKAPDECKS	VCKKCKKNLIISDCEKKGIKINRDV	STANDARD; ; 094298;
233 331 622 187 187 192 192 485 490 493	Similarity 0; Conservat GIHYYYIDGSLL :: GIHEVSVNQSLL EDNNLKIYAK	MSLEQFIKNELYSMODLVEDYKKK E-EFIEKLRGAR- EIEFLKVLYDAEI ALFRYKEFDDELF ALYNKEFDDELF ALYNKEFDE	LIISDC LIISDC 	IN ST 014720; C
DOMAIN DOMAIN MODAES VARIANT VARIANT VARIANT VARIANT VARIANT VARIANT VARIANT VARIANT VARIANT	Ouery Match Best Local S. Matches 120 11 (155 (62)	112 263 263 171 315 213 375 273	419 328 463 373 373 580 639	RESULT 4 K2C1_HUMAN ID K2C1_HUMAN AC P04264; 014720
5-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1-1	on on do	\ \d		RESULT K2C1_H ID K

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284

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348 TTEIDNNIEQISSY-----KSEITELRRNVQALE-----IELQSQLALKQSLEASLA 394
                                                                                                                                                                                                                                                                                                                                  GTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKA----G 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99019489; PubMed-9804344; Smith F.J.D., Maingi C., Covello S.P., Higgins C., Schmidt M., Lane E.B., Uittu J., Leigh I.M., McLean W.H.I. (Gromic organization and fine mapping of the keratin 2e gene (KRT2E): K2e VI domain polymorphism and novel mutations in ichthyosis bullosa
                                                                                                                                                                                                                                            173 FIEKLRGARSEGNNMFQEA-----LIRFRNASSEEMVNAASYLSAALFRYKEFDDEL
                                                                                   290 EMKDLRNVSTGDVNVEMNAAPGVDLTQLLNNMRSQYEQLAEQNRKDAEAWFNEK--SKEL
                                                                                                                             FKKANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFD
                                                                                                                                                                                                                    ECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKIN-RD
                                                                                                                                                                                                                                                                                                     344 VISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATS---TLTGNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-94358459; PubMed-7521371; McLean W.H.I., Morley S.M., Lane E.B., Eady R.A.J., Griffiths W.A.D., Paige D.G., Harper J.I., Higglins C., Leigh I.M.; "Inthhysis bullosa of Siemens -- a disease involving keratin 2e."; J. Invest. Dermatol. 103:277-281(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kremer H., Zeeuwen P., McLean W.H.I., Mariman E.C.M., Lane E.B., van de Kerkhof P.C.M., Ropers H.-H., Steijlen P.M.; "Ichthyosis bullosa of Siemens is caused by mutations in the keratin J. Invest. Dermatol. 103:286-289(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Collin C., Moll R., Kubicka S., Ouhayoun J.-P., Franke W.W.; "Characterization of human cytokeratin 2, an epidermal cytoskeletal protein synthesized late during differentiation.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Keratin, type II cytoskeletal 2 epidermal (Cytokeratin 2e) (K2e)
    244 LRQSVEADI ----NGLRRVLDELTLTKADLEMQIESLTEELAYLKK-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND VARIANTS IBS TYR-192 AND LYS-482.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTSGTTTSSGTGAGGAGSGGPSGHASNA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JARIANTS IBS PRO-187; PRO-490 AND LYS-493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Siemens.";
Invest. Dermatol. 111:817-821(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Thigh epidermis;
MEDLINE=92380238; PubMed=1380918;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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KRT2A OR KRT2E.
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                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions and its long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138 DGGLLSGNEKVTMQNLNDRLASYLDKVRALEESNYELEGKIKEWYEKHGNSHQGEPRDYS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        114 LEQFIKNELYSFSNEIYHTISS-QISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70
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  MICROFIBRILLAR KERATIN: I (ACIDIC; 40-55 kDa) [K9 TO K20] AND II
                   (NEUTRAL TO BASIC; 56-70 kba) [K1 TO K8].
SIMILARITY: BELONGS TO THE INTERMEDIATE FILAMENT FAMILY.
CAUTION: REF. 2 SEQUENCE DIFFERS FROM THAT SHOWN EXTENSIVELY
POSITIONS 513 TO 555.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00226; IF; 1.
Intermediate filament; Coiled coil; Keratin; Disease mutation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 593;
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R -> H (IN EHK).

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R -> C (IN EHK).
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Pred. No. 9.5e-05;
Mismatches 207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001664; IF.
InterPro; IRR02957; Keratin_I.
Pfam; PF00038; filament; 1.
PRINTS; PR01248; TYPEIKERATIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                          SWISS-2DPAGE; P13645; HUMAN.
Aarhus/Ghent-2DPAGE; 7405; IEF
Genew; HGNC:6413; KRT10.
                                                                                                                                                                                                                                                                                                                       M19156; AAAS9468.1; -. M77663; AAAS9199.1; -. L20218; AABS9438.1; -. L20219; AABS9439.1; -.
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MEDLINE-94136477; PubMed-7508181;
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 197-593 FROM N.A.
MEDLINE-92339897; PubMed-1378806;
Tkachenko A.V., Buchman V.L., Bliskovsky V.V., Shvets Y.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 89:910-914(1992)
                                              593 AA.
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MEDLINE=92141228; PubMed=1371013;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92376531; PubMed=1380725;
                                                                                                                                                                                                                                                                                                                                                               Biol. Rep. 12:277-283(1987).
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                                                                                                                                                                                                                                                                 Mol. Biol. 204:841-856(1988).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Science 257:1128-1130(1992).
                                              STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Keratinocytes;
                                                                                                                               Homo sapiens (Human).
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                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_TaxID=9606;
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J. Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                 expression.
                                             K1CJ_HUMAN
P13645:
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                     RESULT 2
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-1. PULNGRPHISM: A NUMBER OF ALLELES ARE KNOWN THAT MAINLY DIFFER IN THE GLY-RICH REGION (POSITIONS 490-560).
-1. DISEASE: DEFECTS IN KRT10 ARE THE CAUSE OF EPIDERMOLYTIC HYPERKERATOSIS OF KRT10 ARE SULLOUS CONGENITAL.
ICHTHYOSIFORM ERYTHRODERMA (BCIE)); A HEREDITARY SKIN DISORDER CHARACPERIZED BY BLISTERING AND A MARKEN THE STRATUM CORNEUM. AT BIRTH, AFFECTED INDIVIDUALS USUALLY PRESENT WITH REDNESS, BLISTERS AND SUPERFICIAL EROSIONS DUE TO CYTOLYSIS. WITHIN A FEW WEEKS, THE ERYTHRODERMA AND BLISTER FORMATION DIMINISH AND HYPERKERATOSES DEVELOP. TRANSMISSION IS AUTOSOMAL DOMINANY, BUT MOST CASES ARE SPORADIC.
-1. DISEASE: DEFECTS IN KRT10 ARE THE CAUSE OF ANNULAR EPIDERMOLYTIC HYPERKERATOSIS (LINICAL AND HISTOLOGIC FEATURES OF BOTH EPIDERMOLYTIC HYPERKERATOSIS CLINICAL AND HISTOLOGIC FEATURES OF BOTH EPIDERMOLYTIC HYPERKERATOSIS AND ICHTHYOSIS BULLOSA OF
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Hohl D., Rothnagel J.A., Roop D.R.;
A novel substitution in keratin 10 in epidermolytic hyperkeratosis.";
J. Invest. Dermatol. 112:506-508(1999).
-!- SUBUNIT: HETEROTETRAMER OF TWO TYPE I AND TWO TYPE II KERATINS.
KERATIN IO IS GENERALLY ASSOCIATED WITH KERATIN 1.
-!- TISSUE SPECIFICITY: SEEN IN ALL SUPRABASAL CELL LAYERS INCLUDING
STRATUM CORNEUM.
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MEDLINE-95059228; PubMed-7526210;
Paller A.S., Syder A.J., Chan Y.-M., Yu Q.-C., Hutton M.E., Tadini G.,
                                                                                                                                                                                                                                            VARIANTS EHK ARG-150; CYS-156 AND GLU-439, AND VARIANT SER-126.
MEDLINE-94216497; PubMed-7512983;
Syder A.J., Yu Q.-C., Paller A.S., Gludice G., Pearson R., Fuchs E.;
"Genetic mutations in the KI and KIO genes of patients with
epidermolytic hyperkeratosis. Correlation between location and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McLean W.H.I., Eady R.A.J., Dopping-Hepenstal P.J.C., McMillan J.R.,
Leigh I.M., Navsaria H.A., Higgins C., Harper J.I., Paige D.G.,
Chipev C.C., Yang J. M., Digiovanna J.J., Steinert P.M., Marekov L., Compton J.G., Bale S.J.;
"Preferential sites in Keratin 10 that are mutated in epidermolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARIANT EHK ASN-160.
MEDLINE-A4117868; PubMed-7507150;
Rothnagel J.A., Longley M.A., Holder R.A., Kuster W., Roop D.R.;
"Prenatal diagnosis of epidermolytic hyperkeratosis by direct gene
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Suga Y., Duncan K.O., Heald P.W., Roop D.R.;
"A novel helix termination mutation in keratin 10 in annul
epidermolytic ichthyosis, a variant of bullous congenital
ichthyosiform erythroderma.";
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J. Invest. Dermatol. 102:24-30(1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequencing.";
J. Invest. Dermatol. 102:13-16(1994).
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J. Clin. Invest. 93:1533-1542(1994).
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MEDLINE-94117870; Pubmed-7507152;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

July 16, 2003, 17:37:24; Search time 29.688 Seconds (without alignments) 702.728 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-853-079-52
2565
1 KRFNEHTDMNGIHYXXIDGS.....AKIPGIMTLTLFALLTFIVN 503

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_40:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description.	P08399 mus musculu		homo	homo	mus m	_				P29229 mycoplasma	P12347 acetabulari	O53553 mycobacteri		P05790 bombyx mori		P46591 candida alb		P03211 epstein-bar			Q03353 drosophila		O53810 mycobacteri					P08673 plasmodium		228	968 equin	3647 homo	homo
SUMMARIES		QI	PHX5_MOUSE	K1CJ_HUMAN	K22E_HUMAN	K2C1_HUMAN	K2C1_MOUSE	PER_DROSR	PER_DROME	SWP1_ENCCU	K1CJ_MOUSE	VLPB_MYCHR	PER_ACEME	YZ08_MYCTU	YQ34_MYCTU	FBOH_BOMMO	YS89_CAEEL	HYR1_CANAL	YA68_MYCTU	EBN1_EBV	CYS4_DICDI	K1CJ_BOVIN	PER_DROMA	WA22_MYCTU	Y747_MYCTU	SPG7_DICDI	PER_DROAN	K1CI_HUMAN	FSH_DROME	CSP_PLACC	APMU_PIG		VGLX_HSVEB	K2C5_HUMAN	K220_HUMAN
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. •	* Query	Match	8.7	8.5	8.5	8.1	7.8	7.8	7.7	7.5	7.5	7.4	7.3	7.2	7.2	7.1	7.0	6.9	6.9	6.9	9.8	6.8	6.7	6.7	6.5	6.4	6.4	6.4	6.4					6.3	
		Score	222	217.5	217	209	201	199.5	196.5	193.5	192	190.5	188.5	185	183.5	182.5	180	176.5	17.6	176	175	174	172.5	171.5	166.5	165	164.5	164.5	164.5	163.5	163.5	163	162.5	161	161
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409 GTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDK----AGTGTSGTTT

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A; Residues: 1-174 <LIW>
A; Cass references: EMBL:X05806; NID:g11316; PIDN:CAA29249.1; PID:g1334349
C; Genetics:
A; Cenome: chloroplast
C; Superfamily: period clock protein; EGF homology
C; Superfamily: period
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Search completed: July 16, 2003, 18:09:58 Job time: 61.3761 secs

QΩ	: 773 NDEMEKFMLKKHRESRGRTGEKSKKSANDTLKMLEYSGPGHGIKRGGSHSWEGEANKPKQ 832	: : : : : : : :
фа	421TSGTTTSSGAASGKAG-TGTAGTTTSSEG-AGSDKAGTGTSGTTTSSGTGA-G 470 	QY 281 KAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKI 340 1 : :
oy B	471 GAGSGGPSGHASNA 484 : : 893 GAGGGGAGAAAA 906	OY 341 N-RDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGN 399 : : :
RESULT KRMSE1 keratin N; Alter C; Speci C; Date: C; Acces	KEMSEI 13 KRMSEI, S9K type I cytoskeletal - mouse N;Alternate names: 59-kDa type I keratin C;Species: Mus musculus (house mouse) C;Species: Mus wasculus (house mouse) C;Accession: A02940	QY 400 GGTESGGTAGTTTSGGTEAGGTSGTTTSSGAASGRAGTGTAGTTTSEGAGSDKAGTGTS 459 I
R; Krieg J. Biol A; Title A; Refer A; Acces A; Molec A; Resid	ate f	SI8654 variant surface antigen vlpB precursor - Mycoplasma hyorhinis N;Alternate names: lipoprotein C;Species: Mycoplasma hyorhinis C;Date: 22-Nov-1993 #sequence_revision 14-Jul-1995 #text_change 21-Jul-2000
A; Note: A; Note: C; Comme forms a C; Comme	betwee s with in the	C;Accession: Sibol4 R;Yogev, D.; Rosengarten, R.; Watson-McKown, R.; Wise, K.S. EMBO J. 10, 4069-4079, 1991 A;Title: Molecular basis of Mycoplasma surface antigenic variation: a novel set of di A;Reference number: S18651; MUID:92097525; PMID:1721868 A;Accession: S18654 A;Accession: S18654
C; Comme C; Genet A; Intro C; Super	residue	A; Residues: 1-174 <pgs> A; Residues: 1-174 <pgs> A; Cross-references: EMBL:X62936; NID:g4495092; PIDN:CAA44709.1; PID:g581323 C; Genetics: A; Gene: vlp8</pgs></pgs>
C; Keywo F; 1-143 F; 1-143 F; 144-4 F; 144-1		A;Genetic code: SGC3 A;Start codon: GTG C;Superfamily: glycine-rich cell wall structural protein 1 C;Keywords: surface antigen F;1-29/Domain: signal sequence #status predicted <sig> F;30-174/Product: variant surface protein vlpB #status predicted <mat></mat></sig>
F; 294-3 F; 310-3 F; 329-3 F; 329-3		Ouery Match Best Local Similarity 35.6%; Pred. No. 0.0014; Matches 53; Conservative 25; Mismatches 58; Indels 13; Gaps 5;
F; 395/R F; 458-5 F; 458-5	egylon: stutter 69/Domain: tail <end> 69/Region: V2 and E2 subdomains</end>	QY 345 ISSYKLLLSTITYIVGAGVEAVTYSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTES 404
Query Ma Best Loo Matches	Query Match 7.5%; Score 192; DB 1; Length 569; Best Local Similarity 22.0%; Pred. No. 0.0053; Matches 111; Conservative 68; Mismatches 192; Indels 134; Gaps 19;	QY 405 GGTAGTTTSSGTBAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGT-TT 463
oy Db	19 GSLLA-SGEVTSVFRYISKEYEEVEHTELAKEHCKKEKCVNVDNIEDNNIKIYAK 71	Qy 464 SSCTGAGGAGSGGPSGHASNAKIPG 488
Qy Db	72 QEKSVYTTPADVAGVSDGFFIRGONLGAVGSVNEQPNTVGMSL 114 : :	RESULT 15 S00273
Qy Db	115 EQFIKNELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYE 171	<pre>period clock protein - Acetabularia mediterranea chloroplast (fragment) C;Species: chloroplast Acetabularia mediterranea C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 20-Jun-2000 C;Accession: S00273</pre>
Qy Db	172EFIEKLRGARSEGNNMFQEALIRFRNASSEEWVNAASYLSAALFRYKEF 220 :	Kil-Weber, M.; de Groot, E.J.; Schweiger, H.G. Mol. Gen. Genet. 209, 1-7, 1987 A;Title: Sequence homology to the Drosophila per locus in higher plant nuclear DNA an A;Reference number: S00273
Qy	221 DDELFKKANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIK 280	A;Accession: S00273 A;Molecule type: DNA

Oy 471 GAGSGPSGHASNA 484	DD . 893 GAGGGGAAAAA. 900 RESULT 12	C:Species: Drosophila melanogaster) C:Species: Drosophila melanogaster C:Species: Drosophila melanogaster C:Species: Drosophila melanogaster C:Species: Drosophila melanogaster C:Date: 19-Nov-1988 #text_change 20-Aug-1999 C:Accession: A26588 \$52942 R:Yu, Q: Jacquier, A.C.; Citri, Y.; Hamblen, M.; Hall, J.C.; Rosbash, M. Proc. Natl. Acdession: Sci. US.S. 84, 784-788, 1987 A:Title: Molecular mapping of point mutations in the period gene that stop or speed u A;Title: Molecular mapping of point mutations in the period gene that stop or speed u A;Title: Molecular mapping of point mutations in the period gene that stop or speed u A;Title: Molecular mapping of point mutations in the period gene that stop or speed u A;Title: Molecular cacid sequence not shown; not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-1218 < YUQ> A;Melano B; Hay	within and among species of t 278 wn; translation not shown AA28776.1; PID:9552117	Note: the nucleotide sequence was submitted Note: clone ME-NJ2 Genetics: Genetics:	nces: riyasse:reginousooo 2; 379/1; 498/1 period clock protein; EGF homology ·	7.7%; Score 196.5; DB 2; Length 1218; Similarity 22.6%; Pred. No. 0.008; 9; Conservative 65; Mismatches 229; Indels 181; Gaps	25 GEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVONIEDNNILKITAKQFKGVVT 78	379	129 INTIDAGE-TENDE LIPRESOALD VARIORILIANDESDECCOLINIEE LEALANDESDE LEALANDES LA 439 TYETVAKKANDES LA 439 TYETVAKANDES LA 439 TYETVAKAND	NATIONAL DESCRIPTION OF THE PROPERTY OF THE PR	543DTVKQEVSRRCQALASFMETLMDEVSRADLKLELPHENELTVSERDSVMLGEIS	597 PHHDYYDSKSSTETPPSYNQLNYNBNLLRFFNSKPYTAPAELDPPKTEPPEPRGTCV	SIGN RIFE EALBOLDING CENTRING VISSELGEDES INTERCONDUCTOR (1 1 1 1 1 1 1 1 1 1	OY 378 ESG-GAGSGTGTSV-SATSTLIGNG-GTESGGTAGTTTSS	Qy 415 420
Db 833 QLTLGTDAIKGAAGSAGGAVGTGGVGGGGGGGGGGGGGGGGTTTSGTGTPG 892	Oy 471 GAGSGGPSGHASNA 484	uit fly (Drosophila melanogaster) r // / / / / / / / / / / / / / / / / /	A; Residues: 1-1218 (CIT) A; Residues: 1-1218 (CIT) A; Cross-references: GB:M30114; NID:g158056; PIDN:AAA28754.1; PID:g158059 A; Note: the authors translated the codon TTC for residue 1108 as Ser, and GAC for residu C; Genetics: A; Genetics: A; Genetics: A; Genetics: A; Cross-references: FlyBase:FBgn0003068 A; Cross-references: FlyBase:FBgn0003068 A; Introns: 32/2; 379/1; 498/1; 1069/3; 1148/3; 1195/3 C; Suberfamily: period clock brotein: EGF honology	Query Match 7.7%; Score 196.5; DB 2; Length 1218; Best Local Similarity 22.6%; Pred. No. 0.008; Matches 139; Conservative 65; Mismatches 229; Indels 181; Gaps 26;	Qy 25 GEVTSNERYISKEYEYEHTELAKEHCKKEKCVNVDNIEDNNLKIYAKOFKSVVT 78	79 TPADV-AGVSDGFFIRGQNLGAVGSVNEQPNTVGMSLEOFIKNELYSFSNE 1 1 1 1 1 1 1 1 1	OY 129 IYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGARSEGN 185	QY 186 NMFQEALIRFRNASSEEWVNAASYLSAALFRYKEFDDELFKKANDNFGRDDG 237 1	OY 238 YDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKA 282 1	QY 283FDECKSNAIILKKKILDNDEDVKINFREMVNEVTCA 318 : : :	QY 319 NTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAV-TVSVSATSNGT 377 ::::	'Qy 378 ESG-GAGSGTGTSV-SATSTLTGNG-GTESGGTAGTTTSS	QY 415 420 Db 773 NDEMEKFMLKKHRESRGRTGEKSKKSANDTLKMLEYSGPGHGIKRGGSHSWEGEANKPKQ 832	OY 421TSGTTTSSGAASGKAG-TGTAGTTTSSEG-AGSDKAGTGTSGTTTSSGTGA-G 470	

us-09-853-079-52.rpr

%; Score 198; DB 2; Length 1079; %; Pred. No. 0.0057;	QY 343 DVISSYKLLLSTITXIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGT 402 : : :
360 GAGVEAVIVSVSATSNGTESGGAGSGTGTSVSATST	OY 403 ESGCTAGTTTSSCTEAGGTSGTTTSSGAASGKAGTGTAGSEGAGSDKAGTGT 458
416 TEAGGTSGTTTSSGAASGKAGTGTA-GTT-TSSEGAGSDKAGTGTSGTTTS	Qy 459 SGTTTSSGTGAGGAGSGGPSGHASNA 484 . .: : : : : :
Oy 465 SGTGAGGAGSGGPSGHASNAKIPG 488	RESULT 10 C26427 period clock protein type C - fruit fly (Drosophila melanogaster) C;Species: Drosophila melanogaster
	C;Date: 19-Nov-1988 #sequence_revision 30-Jun-1991 #text_change 20-Aug-1999 C;Accession: C26427 H.V.; Jacquier, A.C.; Yu, Q.; Hall, J.C.; Baltimore, D.; Rosbash, Nature 326, 42-47, 1987 A;Title: A family of unusually spliced biologically active transcripts encoded by a D A;Reference number: A26427; MUID:87144607; PMID:3102970
catin 10. Subd	A;Molecule Lype: MANA A;Residues: 1-1176
	Query Match 7.7%; Score 196.5; DB 2; Length 1176; Best Local Similarity 22.6%; Pred. No. 0.0077; Matches 139; Conservative 65; Mismatches 229; Indels 181; Gaps 26;
A.Reference number: A38182; MUID:92141228; PMID:11371013 A.Accession: A38182 A.Accession: A38182 A.Accession: A38182 A.Accession: A38182 A.Accession: A38182 A.Accession: A38182	OY 25 GEVTSNERZISKEYEYEHTELAKEHCKKEKCVNVDNIEDNNLKIYAKQFKSVVT 78
A. Residues: 445-561 < KOR> A. Mote: sequence extracted from NCBI backbone (NCBIP:79433) C. Superfamily: cytoskeletal keratin C. Keywords: coiled coil	Qy 79 TPADV-AGVSDGFFIRGONLGAVGSVNEQPNTVGMSLEQFIKNELVSFSNE 128 ::
Query Match 7.7%; Score 197.5; DB 2; Length 561; Best Local Similarity 21.7%; Pred. No. 0.0026; Matches 110; Conservative 74; Misematches 197; Indels 125; Gaps 20;	Qy 129 IYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGARSEGN 185
VTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDNIEDNNLKIYA 7 :	QY 186 NMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDG 237
	Qy 238 YDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKA 282
GEGCEQIYNYEE	QY 283FDECKSNAIILKKKILDNDEDYKINFREMVNEVTCA 318 : : :
173 FIEKLRGARSEGNNMFQEALIRFRASSEEMVNAASYLSAALFRYKEFDDE :	QY 319 NTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAV-TVSVSATSNGT 377 ::::
224 LFKKANDNEGRDGYDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAF	Qy 378 ESG-GAGSGTGTSV-SATSTLTGNG-GTESGGTAGTTTSS
284 DECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKIN-R	OY 415 420 DD 773 NDEMEKFMLKKHRESRGRTGEKSKKSANDTLKMLEYSGPCHGIKRGGSHSWEGEANKPKO 832
Db 387 AETEGRYCVQLSQIQAQISALEEQLQEIRAETECQNTEYQQLTDIKIRLE 436	TSGTTTSSGAASGKAG-TGTAGTTTSSEG-AGSDKAGTGTSGTTTSSGTGA-G

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Ricole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A; Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A; Title: Deciphering the biology of Mycobacterium tuberculosis from the complete geno A; Reference number: A70500; MUID:98295987; PMID:9634230
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C;Superfamily: collagen alpha 1(1) chain; fibrillar collagen carboxyl-terminal homolo
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A;Residues: 1-1079 <COL>
A;Cross-references: GB:ALO22022; GB:AL123456; NID:g3261554; PIDN:CAA17749.1; PID:g292
A;Experimental source: strain H37Rv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical glycine-rich protein Rv3512 - Mycobacterium tuberculosis (strain H37RV) C;Species: Mycobacterium tuberculosis C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000 C;Accession: B70807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 LDGIISEVKAQYDS-----ICQRSKAEAETFYQSKYEEL--QITAGKHGDSVRNTKMEI 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------SNGTES 379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   153 LDPFFENYISILRRKVDSLKSDQSRMESELKNMQDLVEEYRTKYEDEINKRTNAENEFVT 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            || :| | :| 325 SELNRMIQRLRSEIDGCKKQISQIQQNINDAEQRGEKALKDAQNKLNEIEDALSQCKEDC 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               385 ARLICDFQELMNTKLALDMEIGTYKKLLEGEEIRMSGECTPNVSVSVSTSHTSMSGGGSR 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----DDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCA-----NTKFE-
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                                                                                                                                                                                                                                                                                                                                                                       7.8%; Score 199; DB 1; Length 581;
20.3%; Pred. No. 0.0023;
tive 61; Mismatches 158; Indels 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         495 YGGSSGGGSGGSYGGSGGSSGGRRGGSGGGGGGSGGSYGGSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ----ISDCEKKGIKINRDV----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  150 VKHDNYILKKEGEGCEQIYN----YEEFIEKLR--
                                                                                                                                                                                                                                                                 F;420-581/Domain: tail <END>
F;420-439/Region: H2 subdomain
F;440-581/Region: V2 and E2 subdomains
                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 20.3%
6; Conservative
                        F;107-419/Domain: rod <ROD>
F;107-414/Region: coil 1A
F;142-153/Region: linker 1
F;154-254/Region: linker 12
F;255-271/Region: linker 2
F;291-298/Region: linker 2
F;291-398/Region: coil 2A
F;291-398/Region: sinter 7
F;295-419/Region: sinter 7
F;395-419/Region: stutter 7
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Best Local S
Matches 96
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N;Alternate names: 67-kDa type II keratin
C;Species: Wus musculus (house mouse)
C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 20-Mar-1998
C;Accession: A02951
R;Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.
J;Biol. Chem. 260, 7142-7149, 1985
A;Tille: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Haliotis rufescens (California red abalone)
C; Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C; Ccession: T08852
R; Shen, X.; Belcher, A.W.; Hansma, P.K.; Stucky, G.D.; Morse, D.E.
J. Biol. Chem. 272, 32472-32481, 1997
A; Title: Molecular cloning and characterization of lustrin A, a matrix protein from shell A; Reference number: 216496; MUID:98070424; PMID:9405458
A; Recession: T08852
A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:AF023459; NID:g2723361; PIDN:AAB95154.1; PID:g2723362
A;Experimental source: tissue type mantle (shell and pearl nacre); cell type pallial
C;Superfamily: antileukoproteinase repeat homology
C;Keywords: extracellular matrix; extracellular protein
F;1382-1426/Domain: antileukoproteinase repeat homology <ALP>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360 GAGVEAVIVSVSATSNGTESG-GAGSGTGTSV---SATSTLTGNGGTESGGTAGTTTSSG 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       416 TEAGGTSGTTTSSGAASGKA-GTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAG---G 471
                                                                                                             373 TSNGTESGGAGSGT-GTSVSATST-LTGNGGTESGGT-AGTTTSSGTEAGGTSGTTTSSG 429
                                                                                                                                                                                     AASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGT-----GAGGAGSGGPSGHAS 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: A92535; MUID:85207740; PMID:2581964
0.00035;
ches 49;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.8%; Score 200.5; DB 37.6%; Pred. No. 0.006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38; Mismatches
  ed. No. 0.00
Mismatches
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        Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lustrin A - California red abalone
  Best Local Similarity 44.4%;
Matches 55; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-1428 <SHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecule type: mRNA
Residues: 1-581 <STE>
                                                                                                                                                                                                                                                                                          NAKI 486
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                                                                                                                                                                                                                                                                                                                                              249 VAKI 252
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A Map position: 17q12-17q21
A:Introns: 209/3; 237/2; 289/3; 343/3; 458/2; 592/3
A:Introns: 209/3; 237/2; 289/3; 343/3; 385/3; 458/2; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 200/3; 
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N;Alternate names: jasmonate inducible protein

C;Species: Brassica napus (rape)

C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 11-May-2000

C;Accession: T08080

R;Geshi, N.; Brandt, A.

Planta 204, 1998

A;Title: Two jasmonate-inducible myrosinase-binding proteins from Brassica napus L.

A;Reference number: 216340; MUID:98192006; PMID:9530873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --EVA 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LEQFIKNELYSFSNEIYHTISS-QISNSFLIMMSDAIVKHDNYILKKEGEGGEQIYNYEE 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            244 LRQSVEADI----NGLRRVLDELTLTKADLEMQIESLTEELAYLKK------NHEE 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          290 EMKDLRNVSTGDVNVEMNAAPGVDLTQLLNNMRSQYEQLAEQNRKDAEAWFNEK--SKEL 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKIN-RD 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ETEGRYCVQLSQIHAQISALEEQLQQIRAETECQNTEYQQLLD------IKIRLEN 444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        344 VISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATS---TLTGNG 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKA----G 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGGLLSGNEKVTMQNLNDRLASYLDKVRALEESNYELEGKIKEWYEKHGNSHQGEPRDYS 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FIEKLRGARSEGNNMFQEA-----LIRFRNASSEEMVNAASYLSAALFRYKEFDDEL 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 FKKANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFD 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  348 TTEIDNNIEQISSY-----KSEITELRRNVQALE-----IELQSQLALKQSLEASLA 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DGSLLASGEVTS----NFR----YISKEYEYEHTELAKEHCKKEKCVNVDNIEDNNLKIYA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:Y11483; NID:e1023101; PIDN:CAA72271.1; PID:e304150 A;Experimental source: cv. Global; idolate a4; young seedlings A;Note: jasmonate inducible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels 109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 593;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KYYKTIDDLKNQILNLTTDNANILLQIDNARLAADDFRLKYEN--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Score 216.5; DB 1;
; Pred. No. 0.00028;
82; Mismatches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
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A;Molecule type: mRNA
A;Residues: 1-680 <GES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   553 GGSSGGGSGGGYGGGSSG--GHKSSS 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTSGTTTSSGTGAGGAGSGGPSGHASNA 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 216;
        A; Cross-references: GDB:118828; OMIM:148080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 21.8%;
Matches 111; Conservative 8
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A; Residues: 1-593 <RIE>
A; Residues: 1-593 <RIE>
A; Residues: 1-593 <RIE>
A; Cross-references: EMBL:X14487; NID:928316; PIDN:CAA32649.1; PID:928317
A; Cross-references: clone lambda KH10-5
A; Experimental source: clone lambda KH10-5
B; Korge, B.P.; Gan, S.Q.; McBride, O.W.; Mischke, D.; Steinert, P.M.
B; Korge, B.P.; Gan, S.Q.; McBride, O.W.; Mischke, D.; Steinert, P.M.
A; Title: Extensive size polymorphism of the human keratin 10 chain resides in the C-term A; Reference number: A38182; MUID:92141228; PMID:1371013
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A; Molecule type: mRNA
A; Residues: 130-278, 'VY', 281-311, 'I', 313-339, 'V', 341-373, 'R', 375-407, 'O', 409-459, 'RS', 46
56-579, 'P', 581-593 < DARI>-
A, Cross-references: EMBL:M19156; NID: 9186769
A, Note: the sequence from Fig. 3 is inconsistent with the nucleotide sequence from Fig. Shorton, M.Y.; Semat, A. Darmon, M.C.; Vasseur, M.
Submitted to the EMBL Data Library, May 1988
A, Reference number: $14667
A, Accession: $14667
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A; Residues: 452-463, P',465-507, Y', 523-593 <KOR2>
A; Cross-references: PIDN: AAB21314.1; PID: 9244508
A; Note: sequence extracted from NCBI backbone (NCBIP: 79431)
B; Tkachenko, A.V.; Buchman, V.L.; Bliskovsky, V.V.; Shvets, Y.P.; Kisselev, L.L.
Gene 116, 245-251, 1992
A; Title: Exons I and VII of the gene (Kerl0) encoding human keratin 10 undergo structura
A; Reference number: PC1102; MUID: 92339897; PMID: 1378806
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A. Residues: 'G',198-407,'Q',409-450,'G',452-486,491-524,534-593 <TKA>
A. Residues: 'G',198-407,'Q',409-450,'G',452-486,491-524,534-593 <TKA>
A. Cross-references: GB MT7663; NID:9186628; PIDN:AAA59199.1; PID:9186629
A. Experimental source: embryonic skin, clone HK51
B. Darmon, M.Y.: Semat, A.: Darmon, M.C.: Vasseur, M.Mol. Biol. Rep. 12, 277-283, 1987
M.D. Biol. Rep. 12, 277-283, 1987
A. Title: Sequence of a cDNA encoding human keratin No 10 selected according to structura
A. Reference number: S14666; MUID:88122104; PMID:2448602
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A; Residues: 130-278, YV', 281-311, 'I', 313-339, 'V', 341-373, 'R', 375-407, 'Q', 409-459, 'RS', 46
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A;Note: the translated sequence in GenBank entry HUMKRT10A, release 111.0, differs from
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Rieger, M.; Franke, W.W.
J. Mol. Biol. 204, 841-856, 1988
A;Title: Identification of an orthologous mammalian cytokeratin gene. High degree of
A;Reference number: S02158; MUID:89125611; PMID:2464696
A;Recession: S02158
                                                                                                                               580 GSGG-GSKGGSISGGGYGSGGGKHSSGGGGSSSGGGGSSSSVKGSSGEAFGS 638
AFGG--SGGRGSSSSGGGYSSGSSSYGSGGRQSGCRGG-SGGGGSISGGGYGSGGGSGGRY 579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Species: Homo sapiens (man)
;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 10-Dec-1999
:Accession: S02158; C38182; B38182; PC1102; S14666; S14669
                                                                                        GKAGTGTAGTTTSSEGAGS-----DKAGTGTSGTTTSSGTGAGGAGSG---GPSGHASNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Molecule type: DNA
A;Residues: 452-593 <KOR1>
A;Cross-references: PIDN:AAB21315.1; PID:g244509
A;Note: sequence extracted from NCBI backbone (NCBIP:79427)
A;Accession: B38182
A;Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: not compared with conceptual translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              keratin 10, type I, cytoskeletal - human N;Alternate names: cytokeratin 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: GDB: KRT10; KPP
                                                                                                                                                                                                                                                           485 KI 486
                                                                                                                                                                                                                                                                                                                                              SV 640
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A; Note: translation of initiator Met is not shown R; Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R. J. Biol. Chem. 260, 7142-7149, 1985 A; Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67,00 late filament subunits. A; Reference number: A92535; MUID:85207740; PMID:2581964 A; Reference number: A92535 A; Molecule type: mRNA A; Residues: 151-183, K', 185-199, M', 201-204, K', 206-236, S', 238-239, R', 241-356, Y', 358-343, S', 538-643 < STED	Oy 319NTKFEALNDLI
A;Cross-references: GB:M10938; NID:q186787; PIDN:AAA36153.1; PID:g386854 A;Experimental source: tissue neonatal foreskin A;Note: the authors translated the codon CUG for residue 476 as Met R;Chipev, C.C.; Korge, B.P.; Markova, N.; Bale, S.J.; DiGlovanna, J.J.; Compton, J.G.; S Cell T0, 831-828, 1992 A:Title: A lengine-mitation in the HI subdomain of keratin 1 causes enidermal	
	SULT 3 4861
A;Residues: 144-146, 'P', 148-159, 'P', 161-183, 'K', 185-186 CCHT> A;Cross-references: GB:M98776; GB:M1215; GB:M11845; GB:M11846; NID:g1843461 A;Note: sequence extracted from NCBI Dackbone (NCBIP:112784) C;Comment: The cytoskeletal and microfilbrillar keratins are classified into two types, t atin IF protein subunit appears to be a heterotetramer of two type I and two type II procycomment: Keratin 1 is expressed in terminally differentiating epidermis.	<pre>keratin, 67k type II epidermal - human N;Alternate names: cytokeratin 2, CK 2; epidermal cytokeratin 2 C;Species: Homo sapiens (man) C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 28-Apr-1995 C;Accesalion: A44861 C;Accellin, C.; Moll, R.; Kubloka, S.; Ouhayoun, J.P.; Franke, W.W.</pre>
C;Genetics: A;Gene: GDB:RRII A;Gene: GDB:RRII A;Map position: 12q11-12q13 A;Note: defects in this gene may result in epidermolytic hyperkeratosis C;Complex: heterotetramer of two type I, usually keratin 10 (see PIR:RRHU0), and two typ	Exp. Cell Res. 202, 132-141, 1992 A;Title: Characterization of human cytokeratin 2, an epidermal cytoskeletal protein s A;Title: Characterization of human cytokeratin 2, an epidermal cytoskeletal protein s A;Reference number: A44861; MuID:92380238; PMID:1380918 A;Accession: A44861 A;Molecule type: mRNA A;Residues: 1-645 <col/>
	Cross-references Experimental sou Note: the author Note: sequence e Superfamily: cyt Keywords: coiled
F.180-214/Region: coil 1A F.215-226/Region: linker 1 F.227-327/Region: coil 1B F.328-344/Region: linker 12	Query Match 8.5%; Score 217; DB 2; Length 645; Best Local Similarity 22.1%; Pred. No. 0.0029; Matches 120; Conservative 100; Mismatches 200; Indels 122; Gaps 26;
F;34-371/Region: Coll 2A F;372-492/Region: coll 2B F;372-492/Region: coll 2B F;437-K437/Mmain: rail <	Qy 11 GIHYYYIDGSLLASGEVTSNFRYISKEYEHTELAKEHCKNEKCVNVDNI 61
720	. QY 62 EDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGONLGAVGSVNEQPNTVG 111
Query Match 8.6%; Score 219.5; DB 1; Length 643; Best Local Similarity 23.6%; Pred. No. 0.00021; Matches 125; Conservative 76; Mismatches 152; Indels 177; Gaps 28;	112 MSLEQFIKNELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDN-YILKKEGEGCEQIYNY :::::::::::::::::::::::::::::::::::
QY 85 GVSDGFFIRGONLGAVGSVNEQPNTVGMSLEQFIKNELYSFSNEIY 130	171 E-EFIEKLRGARSEGNNMFOEALIRFRNASSEEMVNAASYLSA
QY 131 HTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180 :::: : : : : : : : : : : : :	213 ALFRYKEFDDELFKRANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIENFSD
QY. 181REGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKAN 229	273 VNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALND
OY 230 DNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIENFSDVN 274 :::: :: : :	419 VICTOR TO VYDRATABARGUSERALADARRANDE TAULEERALAGARANEER 328LIISDCEKKGIKINRDV-ISSYKLLLSTITYIUGAGVEAVIVSVSA
QY 275 NTDDIKKAEDECKS-NAIILKKKILDNDEDYKINFREMVNEVTCA 318	

OM protein - protein search, using sw model

July 16, 2003, 17:50:14; Search time 59.3761 Seconds Run on:

(without alignments)
814.396 Million cell updates/sec

US-09-853-079-52 Perfect score:

2565 1 KRFNEHTDMNGIHYYYIDGS.....AKIPGIMTLTLFALLTFIVN 503 Sedneuce:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 segs, 96134422 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 08

Database

PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

STIMMARTES

	. Description	period clock prote	keratin 1, type II	keratin, 67K type		probable myrosinas	lustrin A - Califo	keratin, type II c	hypothetical glyci	1 10, t	cloc	clock	clock		variant surface an	period clock prote	· keratin, epidermal	circadian rhythm p	hypothetical glyci		_		hypothetical glyci	σ	hypothetical glyci		\sim	endo-1,4-beta-qluc	hypothetical glyci	hypothetical glyci
SUMMAKIES	ID	UMMS	KRHU2	A44861	KRHU0	T08080	T08852	KRMS2	B70807	A31994	C26427	A26427	A26588	KRMSE1	S18654	S00273	807330	A25018	D70807	F70806	S66852	F70963	E70806	A43855	A70934	T28125	S58135	E82759	C70974	B70893
	DB	-	П	~	Н	~	~1		~	7														7	7	7	7	7	7	7
	Length	713	643	645	593	680	1428	581	1079	561	1176	1218	1218	269	174	174	570	1127	1489	1901	967	778	1381	1536	1306	2329	937	592	731	463
ф	Query Match	8.7	8.6	8.5	8.4	8.4	7.8	7.8	7.7	•	7.7	7.7		7.5	7.4	7.3	7.3	7.3	7.3	7.2	7.2	7.2	•	•	•	7.0	•		6.9	•
	Score	222	219.5	217	216.5	216	200.5	199	198	197.5	196.5	196.5	196.5	192	190.5	188.5	188.5	186	186	185	184	183.5	183.5	182.5	181	18	178.5	178	177	176
	Result No.	1	7	e	٧.	2	9	7	80	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

hypothetical glyci	nuclear antigen EB	hypothetical prote	period clock prote	hypothetical glyci	hypothetical prote	keratin, 54K type	hypothetical glyci	glycine-rich prote	keratin, 70k type	period clock prote	1,4-beta-cellobios	sericin1B - silkwo	hypothetical prote	secreted acid phos	hypothetical glyci	
D70916	QQBE31	877300	B26427	H70846	T33913	KRBOVI	D70931	T49109	A60830	UMFF	A82704	S52714	F75518	T46726	н70987	
7	Н	7	7	7	7	7	~	7	7	Т	7	~	7	7	7	
491	641	3016	1122	1538	605	526	639	396	270	571	683	1217	839	888	914	
6.9	6.9	6.9	6.8	9.9	8.9	9.9	9.9	8.9	6.7	6.7	6.7	6.7	6.7	6.7	6.7	
176	176	176	175.5	175.5	175	174	174	173.5	173	173	173	173	172.5	172	171.5	
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	

ALIGNMENTS

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C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jun-2000
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jun-2000
C:Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 16-Jun-2000
C:Accession: A24403
R:Shin, H.S.; Bargiello, T.A.; Clark, B.T.; Jackson, F.R.; Young, M.W.
Nature 317, 445-448, 1985
A;Title: An unusual coding sequence from a Drosophila clock gene is conserved in vert A; Reference number: A24403 MUID:86014384; PMID:2413365
A;Accession: A24403
A;Accession: A24403
A;Accession: A24403
A;Accession: A24403
A;Residues: 1-713 <cmtobal A;Accession: A24403
A;Residues: 1-713 <cmtobal A;Accession: A24403
A;Cross-references: GB:MI20366; GB:MI2039; NID:955125; PIDN:CAA26710.1; PID:91334150
C;Comment: Mutations within the per locus of the fruit fly affect a variety of natura logous locus with multiple tandem repeats of nucleic acid hexamers (ACNGGN, TCAGGC) t C;Comment: The serine residues of the S-G repeats found in certain proteoglycans are C;Comment: The serine residues of the S-G repeats found in certain proteoglycans are C;Comment: The serine residues of the S-G repeats found in Certain proteoglycans are C;Comment: The serine residues of the S-G repeats found in Certain proteoglycans are C;Comment: The serine residues of the S-G repeats found in Certain proteoglycans are C;Comment: The serine residues of the S-G repeats found in Certain proteoglycans are C;Comment: The serine residues of the S-G repeats found in Certain proteoglycans are C;Comment: The serine residues of the S-G repeats found in Certain proteoglycans are C;Comment: The serine residues of the S-G repeats found in Certain proteoglycans are C;Comment: The S-G repeat repeat

9 Gaps 26; 8.7%; Score 222; DB 1; Length 713; 41.7%; Pred. No. 0.00018; tive 16; Mismatches 46; Indels ; 63; Conservative Similarity Query Match Best Local S Matches 63

360 GAGVEAVTVSVSATSNGTESG-----GAGSGTGTS-VSATSTLTGNG-GTESGGTA 408 ð q

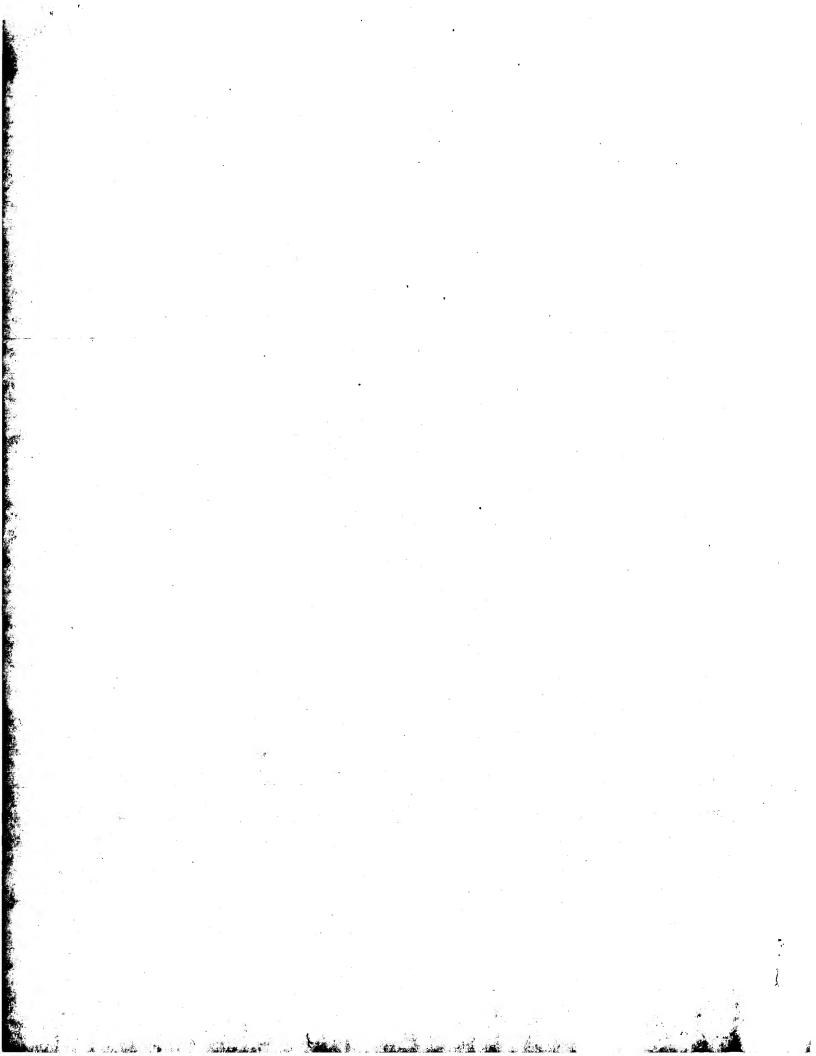
409 GTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDK-----AGTGTSGTTT 463 ò

g

464 SSGTGAG-GAGSGGPSGHASNAKIPGIMTLT 493 δ

qq

National I, type II, cytoskeletal - human
N;Alternate names: 67K type II epidermal keratin; cytokeratin I
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1966 #sequence_revision 22-Oct-1999 #text_change 10-Dec-1999
C;Accession: A22940; A02950; A43342
K;Johnson, L.D.; Idler, W.W.; Zhou, X.M.; Roop, D.R.; Steinert, P.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 1896-1900, 1985
A;Reference number: A22940; MuID:85166239; PMID:2580302
A;Accession: A22940
A;Molecule type: DNA
A;Residues: 1-643 <-JOH>
A;Residues: 1-643 <-JOH>
A;Cross-references: GB:M98776; GB:M1215; GB:M1845; GB:M11846; NID:g1843461



us-09-853-079-52.rapb

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SEGNNMFQEALIR-FRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF 240
                                                                                                                                             DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
                                                                                                                                                                                                                      DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYI-- 358
                                                                                                                                                                                                                                           80 PADVAGVSD--GFFIRGONLGAVGSVNEQPNTVGMSLEQFIKNELYSFSNEIYHTISSQI 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 SEGNNMEQEALIR-FRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
 ---LKKEGEGCEQIYNYEEFIEKLRGAR 181
                                                                                               DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYI-- 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  138 SNSFLIMMSDAIVK-----HDNYI------LKKEGEGCEQIYNYEEFIEKLRGAR 181
                     75 PSEAGGPSEAGGPSGTGSEAGGWPSGTGWPSEAGWSSERF-GYQLLPYSRI--VIFNEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HOWEL, MALY ABOUT SECTIST, HOLLOWIS, SECTIST, HOLLOWIS, SECTIST, HOLLOWING AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FASTSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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138 SNSFLIMMSDAIVK-----HDNYI--
                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 49, Application US/09853079
Publication No. US20030109689A1
                                                                                                                                                                                                                                                                                                                     342 ITKVSNVIIPGIKALTLTV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: MONeill, Paul R.
APPLICANT: HOMEY, MARY
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US-09-853-079-49
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Db 342 ITKVSNVIIPGIKALTLTV 360
Search completed Inlv 16 2003 18 08 38

Search completed: July 16, 2003, 18:08:38 Job time : 84.2782 secs

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US20010029295A1
                                                                                                           APPLICANT: Homer, Mary
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                                                                                                                                                                                                                                                                                          ORGANISM: Babesia
                                                                                                                                                                                                                                                                                                         US-09-737-178-144
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US-09-286-488-49
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                                                                                                       274 NNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDC 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             396 LTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           570 LTGNGCTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAG 629
                                                                                                                         STLTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDK
                                                                              Gaps
                                                                                                                                                                                                                                                                                                          454 AGTGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREPTMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C11
                                                                            Indels
                                            Score 1143; DB 10;
Pred. No. 1.8e-65;
2; Mismatches 0;
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CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 144
LENGTH: 677
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 144, Application US/09853079
Publication No. US20030109689A1
GENERAL INFORMATION:
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US-09-737-178-144
; Sequence 144, Application US/09737178
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Sleath, Paul R.
APPLICANT: MCNeill, Patricia D.
APPLICANT: Homer, Mary
                                              44.6%;
99.1%;
                                            Query Match
Best Local Similarity 99.13
Matches 228; Conservative
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US-09-853-079-144
; ORGANISM: Babesia
US-09-737-178-85
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US-09-853-079-144
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Best Local S
Matches 228
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450 TDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMYNEYTCANTKFEALNDLIISDCEK 509
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APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R:
APPLICANT: Sleath, Paul R:
APPLICANT: Sleath, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210.12.1.426.3
CURRENT APPLICATION NUMBER: US/09/286,488
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 83
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  456 TGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 677;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 367;
                                                                                                                                 APPLICANT: Secrist, Heather TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: COMPOUNDS AND METHOD B. MICROTI INFECTION FILE REFERENCE: 210121.426C9 CURRENT APPLICATION NUMBER: 02/09/737,178 CURRENT FILING DATE: 2000-12-13 NUMBER OF SEQ ID NOS: 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1141; DB 10;
Pred. No. 2.5e-65;
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28.8%; Pred. No. 2.5e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                            44.5%; Scc. 100.0%; Pred. No. ... 0. Mismatches
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Patent No. US2002016913641
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
                                             ij
                                                                   Sleath, Paul R.
McNeill, Patricia D.
Reed, Steven G.
Lodes, Michael J.
Houghton, Raymond
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Best Local Similarity 100.
Matches 228; Conservative
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US-09-286-488-49
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274 NNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDC 333
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                                  Gaps
   447 EGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Monill, Paul R.
APPLICANT: Moner, Mary
APPLICANT: Moner, Mary
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS;
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.42669
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000.12-13
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                              JULIARY INFORMATION:

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Lodes, Michael J.

APPLICANT: Gloughton, Raymond L.

APPLICANT: Houghton, Raymond L.

APPLICANT: Houner, Mary

APPLICANT: Houner, Mary

APPLICANT: Houner, Heather

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS

TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION

FILE REFERENCE: 21012.1 456C1

CURRENT APPLICATION NUMBER: US/09/853,079

CURRENT FILING DATE: 2001-05-09

NUMBER OF SEQ. ID NOS: 224

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 85

TOWNEY OF SEX OF
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                                                                                                                                                                                                            Sequence 85, Application US/09853079; Publication No. US20030109689A1; GENERAL INFORMATION:
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; Patent No. US20010029295A1
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Matches 228; Conserv
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                                                                                                                                                                                      US-09-853-079-85
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LENGTH: 666
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                                                                                           DLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGT
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APPLICANT: Lodes, Michael J.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Momer, Mary
APPLICANT: Homer, Mary
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C9
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT APPLICATION NUMBER: US/09.737,178
CURRENT FILLING DATE: 2000-12-13
NUMBER OF SEQ ID NOS: 144
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45.2%; Score 1159.5; DB 10; Length
58.3%; Pred. No. 3e-66;
ive 35; Mismatches 89; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 87, Application US/09737178 Patent No. US20010029295A1
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Lodes, Michael J.
Houghton, Raymond L.
Sleath, Paul R.
MONeill, Patricia D.
Homer, Mary
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Best Local Similarity 58.3%
Matches 278; Conservative
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APPLICANT: Reed, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; TYPE: PRT
; ORGANISM: Babesia
US-09-737-178-87
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                                                       ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180
                                                                                                                                                                                                                                                                                                            DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG 360
   73 KRENEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN 132
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APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Parricia D.
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROIL INFECTION
FILE REFERENCE: 210121.426C11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45.2%; Score 1159.5; DB 9; Length
58.3%; Pred. No. 3e-66;
ive 35; Mismatches 89; Indels
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CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence 87, Application US/09853079; Publication No. US20030109689A1; GENERAL INFORMATION:
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278; Conservative
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US-09-853-079-87
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Bleath, Paul R.
APPLICANT: Moneill, Paul R.
APPLICANT: Homer, Mary
APPLICANT: Georist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIACNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.42699
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
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Pred. No. 6.9e-129;
); Mismatches 2;
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FastSEQ for Windows Version 3.0
                                     Windows Version 3.0
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Patent No. US20010029295A1
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99.5%;
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Best Local Similarity 99.5%
Matches 417; Conservative
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Best Local Similarity 99.5
Matches 417; Conservative
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ORGANISM: Babesia microti
                                                                                                   ORGANISM: Babesia microti
CURRENT FILING DATE:
NUMBER OF SEQ ID NOS:
SOFTWARE: FASTSEQ for
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SOFTWARE: FastSEQ fo
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                                                                                     TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 452;
                                                                                                                                                                                                                                               FILE REFERENCE: 210121.426C11
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
SOFTWARE OF SEQ ID NOS: 224
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                                                                                                                                                            APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Homer, Mary
APPLICANT: Homer, Mary
APPLICANT: Homer, Mary
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE
                                                                                                                                                                                                                                                                                                                               SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 209
                                                   ASNAKIPGIMILILFALLTFIVN 503
                                                                                                                          Sequence 209, Application US/09853079
Publication No. US20030109689A1
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US-09-853-079-209
                                                                                                                                                   GENERAL INFORMATION
                                                                                                  RESULT 4
US-09-853-079-209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 492;
                                       GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Bleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: Steath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROII INFECTION FILE REFERENCE: 210121.4263
CURRENT APPLICATION NUMBER: US/09/286,488
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C11
CURRENT APPLICATION NUMBER: US/09/853,079
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Pred. No. 6.9e-129;
0; Mismatches 2;
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SOFTWARE: FastSEQ for Windows Version 3.0
  US/09286488
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: MONeill, Patricia D.
APPLICANT: Homer, Mary
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99.5%;
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US-09-286-488-21
Sequence 21, Application UP Patent No. US20020169136A1
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                                                 TSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGH
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                              AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGG
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APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.
APPLICANT: McNeill, Patricia D.
APPLICANT: Secrist, Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121,42669
CURRENT APPLICATION NUMBER: US/09/737,178
CURRENT FILING DATE: 2000-12-13
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SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                     ; Sequence 52, Application US/09737178
; Patent No. US20010029295A1
; GENERAL INFORMATION:
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Matches 503;
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APPLICANT: Lodes, Michael J.
APPLICANT: Hodes, Michael J.
APPLICANT: Houghton, Raymond'L.
APPLICANT: Houghton, Raymond'L.
APPLICANT: Houner, Mary
APPLICANT: Honeill, Patricia D.
APPLICANT: Honeill, Patricia D.
APPLICANT: Honer, Mary
APPLICANT: Honer, Mary
APPLICANT: Heather
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426c11
CURRENT APPLICATION NUMBER: US/09/853,079
CURRENT FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                                                                                                                                                               Sequence 52, Application US/09853079 Publication No. US20030109689A1 GENERAL INFORMATION:
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Matches 503; Conservative
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1 KRENEHTDMNGIHYYYIDGS .....AKIPGIMTLTLFALLTFIVN
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/cgn2_6/ptcdata/2/pubpaa/NS06_NEW_PUB.pep:*
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/cgn2_6/ptcdata/2/pubpaa/US10_PUBCOMB.pep:*
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                       GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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9 US-09-853-079-52

10 US-09-873-079-52

9 US-09-873-079-209

9 US-09-886-488-21

10 US-09-737-178-21

9 US-09-853-079-87

10 US-09-853-079-85

10 US-09-853-079-85

10 US-09-737-178-85

10 US-09-737-178-85

10 US-09-853-079-144

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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Maximum DB seq length: 2000000000
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Sequence 144, App Sequence 49, Appl Sequence 49, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl Sequence 20, Appl

US-09-737-178-20

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Sequence 136, App Sequence 208, App Sequence 208, App Sequence 3, Appli Sequence 3, Appli Sequence 24, Appl Sequence 24, Appl Sequence 107, App Sequence 107, App Sequence 207, App Sequence 155, App Sequence 155
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Patent No. US20020169136A1
Batent No. US20020169136A1
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: MCNoill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: UNMBER: 1909-04-05
CURRENT FILING DATE: 1999-04-05
SOFTWARE FESTSED for Windows Version 3.0
SEQ ID NO 52
LENGTH: 503
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Pred. No. 9.3e-157;
Mismatches 0;
                  US-09-853-079-121

0 US-09-737-178-121

US-09-737-178-136

US-09-737-178-136

US-09-737-178-136

US-10-123-155-3

US-10-146-731-3
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US-09-286-488-24
US-09-853-079-24
US-10-184-644-107
US-10-184-644-107
US-10-184-644-207
US-10-184-644-207
US-10-184-644-207
US-10-184-644-207
US-10-184-644-207
US-10-184-644-207
US-10-184-634-207
US-10-184-634-207
US-10-184-634-417
US-10-184-644-417
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ORGANISM: Babesia microti
Query Match
Best Local Similarity
121
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914 AA; 100583 MW; 7E7A9B3A5BAA53C2 CRC64;

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SEQUENCE
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
CDNA FL131022 fis, clone NT2RP3000753, weakly similar to neurofilament
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Ota T., Suzuki Y., Obayashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y., Isogai T., Sugano S.; "NEDO human cDNA sequencing project."; Nawamura Y., Isogai T., Sugano S.; Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AK000561; BAA91111.1; - Interpro; IPR000591; DEP.
SMART: SM00049; DEP.
PROSITE: FS50186; DEP: 1.
PROSITE: FS50186; DEP: 1.
                                                                                                                                                                                                                                 Gaps
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Washaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                         Score 36; DB 11; Length 465;
Pred. No. 34;
4; Mismatches 15; Indels
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52;
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Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF290208; AAL27891.1; -.
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"NEDO human cDNA sequencing project.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AK023084; BAB14396.1;
                                               EMBL; AF290205; AAL27891.1; JOINED.
EMBL; AF290206; AAL27891.1; JOINED.
EMBL; AF290207; AAL27891.1; JOINED.
SEQUENCE 465 AA; 49160 WW; 52A263D653DA8F80 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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26.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tormo M.A., Cucarella C., Amorena B., Lasa I., Penades J.R.;
"The Bap Homolog Protein of Staphylococcus epidermidis RP62A Promotes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
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                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus epidermidis.
Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33.3%; Score 36; DB 2; Length 2402;
41.2%; Pred. No. 1.9e+02;
tive 2; Mismatches 8; Indels
                      Length 914;
                                                             8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D5807D96B8F2E9CC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AY028618; AAK29746.1; -
InterPro; IPR001298; Filamin.
                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam: PF00746; Gram_pos_anchor; 1.
Pfam: PF00746; HYR: 1.
Pfam: PF00801; PF05: 1.
TIGRFAMS; TIGR01167; LEXTG_anchor; 1.
TIGRFAMS; TIGR01168; VSIRK_signal; 1.
PROSITE; PS00343; FILANI_REPEAT; 2.
PROSITE; PS0343; GRAM_POS_ANCHORING; UNKNOWN_1.
SEQUENCE 2402 AA; 258095 MW; D5807D96B8F2E9C
                 Score 36; DB 4;
Pred. No. 69;
2; Mismatches 6
                                                                                                                                                                                                                                                         PRT; 2402 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001899; Gram_pos_anchor.
InterPro; IPR003410; Hyalin.
InterPro; IPR000601; PKD_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: July 16, 2003, 17:50:01 Job time: 9.77066 secs
                                                                                                                                                                                                                                                                                                 Created)
                                                                                                     4 KXNXNKSXXAXXKSXDTQ 21
                                                                                                                                  125 KSADTQTTNETTNKNDD 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16 KSXDTQTXQEXXXXEE 32
                                                                                                                                                                                                                                                                         Ogher7;
Ol-JUN-2001 (TrEMBLrel. 17,
                                          44.48;
Query Match
Best Local Similarity 44.4%
Best Local Similarity 64.4%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 41.2.
                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                 Bap-like protein Bhp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biofilm Formation."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=1282;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-RP62A;
                                                                                                                                                                                                                                                         09AER7
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Adams No. Cellifers S.E., Holf R.A., Evans C.A., Gocayne J.D.,
Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
R.A Adamstides D.G., Scherer S.E., Holf R.A., Evans C.A., Gocayne J.D.,
R.A. George R.A. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
R.A. Burtanon R.C., Ragers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
R.A. Abril J.E., Apbayani A., An H.-J., Andrews-Fehankoch C., Baldwin D.,
Ballew R.M., Basu A., Barman B.P., Bhandari D., Belshakov S.,
Ballew R.M., Basu A., Barman B.P., Bhandari D., Belshakov S.,
Baltew R.M., Cavley S., Dallker C., Davenport L.B., Davies P.,
R.A. Cherry J.M., Cavley S., Dallker C., Davenport L.B., Davies P.,
R.A. Cherry J.M., Cavley S., Dallker C., Davenport L.B., Davies P.,
R.A. Durbin K.J., Evangelista G.C., Ferraz C., Ferriera S., Fleischmann W.,
R.A. Baris N. Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
Burtis N.D., Doup L.E., Garuy N.S., Gelbart W.M., Glasser K.,
Aldek A., Gong F., Gorrell J.H., Guz Z., Kennison J.R., Netchun M.,
R.A. Harris N.L., Harvey D., Helmann T.J., Hernandez J.R., Houck J.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.R., Netchun M.S.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.R., Netchun H.,
R.A. Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.K.,
R.A. Rankerl B., McIntosh T.C., McLeod M.P., McPherson D.,
R.A. Mount S.M., Moy M., Murphy B., Winderson D., Wolferson R.A., Moy M., Nurbhy B., Nordeson M., Strong R., Sun E.,
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
R. Wasarman D.A., Walnistcock G.M., Welssenbach J.,
R. Wasarman D.A., Walnistcock G.M., Welssenbach J.,
R. Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Zho Q.A.,
Ye H., Yen Senger E., Stapleton M., Strong R., Saint T.,
R. Yang S., Wasarman D.A., Walnistcock G.M., Welssenbach J.C.,
R. The genome sequence of Drosophila melanogaster "."
R. Science 287:2185-2195(2001)
R. Wells A., Woll W., Woll W., Woll W., Woll W., Strong S., S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ;
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Pred. No. 29;
3; Mismatches 19; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              45117 MW; 71CA68B1D6B50E3F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         317 HEFPNRNEEDQATRRSESTSTQAETGPQTQE 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 HXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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  MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0039267; CG13649.
InterPro; IPR003889; FYrich_C.
InterPro; IPR003888; FYrich_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33.3%;
29.0%;
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20,
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Best Local Similarity 29.v.
9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Podocalyxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00542; FYRC;
SMART; SM00541; FYRN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=129/SVJ;
Kershaw D.B., Li J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q8VIQ4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q8VIQ4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PODXL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Favello A., Fulton L., Gattung S., Greco T., Kirsten J., Kucaba T., Hallsworth K., Hawkins J., Hiller L., Jier M., Johnson D., Johnston L., Largaton Y., Latrelle P., Le T., Mardis E., Menezes S., Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L., Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Vaudin M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBL_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13; Indels
                      Verhasselt P., Volckaert G.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

EMBL; X89514; CAA61704.1; -.

EMBL; X91258; CAA62637.1; -.

EMBL; 273288; CAA97655.1; -.

EMBL; U53877; AAB82372.1; -.
                                                                                                                               Delius H.;
Submitted (SEP-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wilson R., Waterston R.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                            SEQUENCE FROM N.A.
Delius H., Hebling U.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                    Pauley A.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: Ifnoveror.
Pfam; PF00117; GATase; 1.
Glutamine amidotransferase; Transferase.

$\frac{1}{2} \text{ for 2892} \text{ FCC9648B62880D5C CRC64;}$
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GHPEFNSDVAQKGLLKSQDKLTLEE 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GHXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S0004116; YLR126C.
rPro; IPR000991; GATase_1.
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32.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 32.03
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
STRAIN-FY23 /RD005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                    SEQUENCE FROM N.A. STRAIN=S288C;
                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-S288C;
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Gaps

RESULT 11 Q9VBY9

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us-09-853-079-39.rspt

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Conservative
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                                                                                                                                                    Query Match
Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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tes 9; Conserv
                                                                                                                                         608 AA;
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                     Ephydroidea; Dro:
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-BERKELEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Celniker S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     115
                                                                                                                              PRINTS; P
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                                                                                                                                                                                                                                                                                             Q8SZ45
Q8SZ45;
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                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAINEL TOR NI6961 / SEROTYPE 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Elsen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (Mouse-ear cress).
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN=COLUMBIA;
Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                          "DNA sequence of both chromosomes of the cholera pathogen Vibrio
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0
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0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16; Length 290;
13;
 Length 241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13; Indels
                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      290 AA; 32611 MW; 2E3CC4062C2055E5 CRC64;
                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Genomic DNA, chromosome 3, BAC clone: T19N8.
 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           608 AA
DB :
                                                                                                                              290 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pred. No. 13;
            ed. No. 11;
Mismatches
                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence
01-JUN-2002 (TrEMBLrel. 21, Last annotat:
Pseudouridine synthase family 1 protein.
Score 37;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00849; Pseudou synth 2; 1.
TIGRFAMs; TIGR00093; Cons_hypoth93; 1.
PROSITE; PS01149; PSI_RSU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR004397; Cons_hypoth93.
InterPro; IPR000613; PseudoU_synth.
InterPro; IPR000748; Psi_RSU.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GHPPTRANRKSVANKKKNATQT 100
                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                             1 GHXKXNXNKSXXAXXKSXDTQT 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GHXKXNXNKSXXAXXKSXDTQT 22
                                                                   GHPPTRANRKSVANKKKNATOT 51
                                                                                                                                                                                                                                                                                                                                                                                                  Nature 406:477-483(2000).
EMBL; AE004194; AAF94299.1; -.
34.3%;
36.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        36.48;
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Matches 8; Conservative
                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complete proteome. SEQUENCE 290 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3702;
                                                                                                                                                                                                             Vibrio cholerae.
                                                                                                                                                                                                                                  NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                           TIGR; VC1140;
                                                                                                                                                                                                                                                                                                                                                                  Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                        cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9LH95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09LH95
                                                                                                                                         O9KSW6
                                                                                                                            09KSW6
                       Matches
                                                                                                     RESULT 7
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Q9LH95
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                                                    Nakamura Y.;
"Structural analysis, of Arabidopsis thaliana chromosome 3. II.
"Structural analysis, of Arabidopsis thaliana chromosome 3. II.
"Structural analysis, of the regions of 4,251,695 bp covered by ninety Pl,
TAC and BAC clones.";
DNA Res. 7:217-221(2000).
EMBL; AP002057; BAB03177:1;
InterPro; IPR002055; P.rich extensn.
PRINTS; PR01217; PRICHEXIENSN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J., Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E., George R., Gonzallez M., Guaralin H., Kronmiller B., Li P., Liao G., Miranda A., Mungall C.J., Nunco J., Pacleb J., Paragas V., Park S., Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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                                                                                                                                                                                                                                                                                                                                                        Length 608;
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                                                                                                                                                                                                                                                                                                                                                                                                            13; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL, AY071126; AAL48748.1; -SEQUENCE 198 AA; 22012 MW; CE33F831FAB79D49 CRC64
                                                                                                                                                                                                                                                                                             6C6368AF4BD2A3B9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
ORF YLR126C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                     ore 37; DB 10;
ed. No. 28;
Mismatches 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | : | : | : | HEFPINREEDQATRRSESTSTQAETGPQTQE 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 HXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33.3%; Score 36; DB 29.0%; Pred. No. 14; iive 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                     34.3%; Score 37; 29.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLR126C OR L3105 OR L3101 OR L9233.12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              429 NSKSSSSSSSTTSVKEVETQTSSE 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 HXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
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STRAIN-COLUMBIA;
MEDLINE-20363099; PubMed-10907853;
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                                                                                                                                                                                                                                                                                             62766 MW;
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STRAIN=569B;
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SEQUENCE
                                                                                                 subtilis
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Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
A Boriss R., Boursler L., Brans A., Braun M., Brignell S.C., Bron S.,
Bronillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,
Brian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
A Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
A Hilbert H., Holsappel S., Haga K., Halech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarerto V.,
A Kurita K., Lapidus A., Lardinois S., Mauel C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Mosell D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
A Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sato T., Scanlan E., Pauli E., Rapport G., Rey M., Tamakoshi A., Tarakenin K., Takamaka P., Tarkamashi H., Takemaru K.,
A Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tanconi E., Takamashi H., Takemaru K.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., SEQUENCE OF 27-37 AND CHARACTERIZATION.
MEDIINE-99140137; Pubmed=10206711;
Margot P., Pagni M., Karamata D.;
"Bacillus subtilis 168 gene lytF encodes a gamma-D-glutamate-meso-diaminopimelate muropeptidase expressed by the alternative vegetative
                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Endopeptidase LYTF precursor (Cell wall-associated polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
Bacillaceae; Bacillus.
NCBL_TaxID=1423;
                                                                                                                                                                                                                                                                                                                  Length 1033;
                                                                                                                                                                                                                                                                                                                                                           11; Indels
                                                                                                                                                                                                                                                                   1033 AA; 114266 MW; 559659540BDE66F5 CRC64;
                                                                                                                                                                                                                ATP-binding; Immunoglobulin domain; Transferase;
Tyrosine-protein kinase.
SEQUENCE 1033 AA; 114266 WW; 559659540BDE66F
                                                                                                                                                                                                                                                                                                               DB 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         488 AA.
                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                             Score 38.5;
Pred. No. 24
                                                                  Prodom; PD000001; Euk_pkinase; 1.
SMART; SM00408; IGc2; 3.
SMART; SM00410; IG_like; 2.
SMART; SM00219; TyrKc; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                          648 GHSK-SRSKSSGDAQKSDDTACSQQ 671
                                                                                                                                                                                                                                                                                                                                                                                                          1 GHXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Created)
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Microbiology 145:57-65(1999).
                                                                                                                                                                                                                                                                                                               35.6%;
40.0%;
                                              PRINTS; PR00109; TYRKINASE
Pfam; PF00047; ig; 5.
Pfam; PF00069; pkinase; 1.
                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 40.0
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1997 (TrEMBLrel. 01-JUL-1997 (TrEMBLrel. 01-JUN-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                               Query Match
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Noback M.A., Terpstra P., Holsappel S., Venema G., Bron S.; Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: D-GLUTAMATE - M-DIAMINOPIMLATE ENDOPEPTIDASE. CELL WALL HYDROLASE INVOLVED IN CELL AUTOLXSIS.
-!- SUBCELLULAR LOCATION: CELL-WALL BOUND.
-!- SIMILARITY: BELONGS TO THE E.COLI NLPC / LISTERIA P60 FAMILY.
Viari A., Wambutt R., Wedler B., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.; "The complete genome sequence of the gram-positive bacterium Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vibrio cholerae.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                          Kunst F., Ogasawara N., Yoshikawa H., Danchin A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF261151, AAG16128.1; -.
InterPro; IPR004397; Cons_hypoth93.
InterPro; IPR006613; Pseudod_synth.
InterPro; IPR006748; Psi_RSU.
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TIGRRAMS; TIGR00093; Cons_hypoth93; 1.
PROSITE; PS0149; PS1_RSU; 1.
PROGINCE 241 AA; 26964 WW; F12D39E90911079F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            6FE0E96A4B42BDC8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. 16, Created)
1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Pseudouridylate synthase-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
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Pred. No. 14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
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POLY-SER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEROPS; C40.002; -. InterPro; IPR002482; LysM. InterPro; IPR00064; NLPC_P60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01476; LysM; 5.
Pfam; PF00877; NLPC_P60; 1.
SMART; SM00297; LysM; 5.
Cell wall; Hydrolase; Repeat; SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51397 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y14079; CAA74437.1; -. EMBL; Z99109; CAB12776.1; -.
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36.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 30.0.
7; Conservative
                                                                                                                         Nature 390:249-256(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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488
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163
172
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288
305
355
488 AA;
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Length 1033;

DB 5;

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SEQUENCE FROM N.A.
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NCBL_TaxID=7227;
                                                                                                                                                                                                                                             CG8967.
                                                                                                                                                                                                                                OTK protein.
OTK OR CG896
   Query Match
                                                                                                                                                         09V643
09V643;
                                                                                                                               RESULT 4
                                                                                                                                               Q9V643
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0
                                                                                                                           Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L.D., Benson D.R., Krause P.J., Reed S.G., Persing D.H.; "Serological expression cloning of novel immunoreactive antigens of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila,
                                                                                                                                                                                                                                                                                                                      Gaps
                                           Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pulido D., Campuzano S., Koda T., Modolell J., Barbacid M.;
"Dtfk, a Drosophila gene related to the trk family of neurotrophin
receptors, encodes a novel class of neural cell adhesion molecule.";
EMBO J. 11:391-404(1992)
                                                                                                                                                                                                                                                                                                                    .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00408; IGC2; 3.
SMART; SM00410; IG_11ke; 2.
SMART; SM00219; TYPKC; 1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00109; PROTEIN_KINASE_TYR; 1.
ATP-binding; Cell adhesion; Immunoglobulin domain; Signal;
                                                                                                                                                                                                                                                                                        Length 275;
                                                                                                                                                                                                                                                                                                                    14; Indels
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W; D282EFCB28ACA8D0 CRC64;
                                                                                                                                                                                                                                            275
30775 MW; C3CC5D5EBC494E01 CRC64;
01-OCT-2000 (TrEMBLrel. 15, Last annotation update) Seroreactive antigen BMN1-20 precursor (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                     73.1%; Score 79; DB 5; I
56.2%; Pred. No. 2.4e-08;
tive 0; Mismatches 14;
                                                                                                                                                                                                                                                                                                                                                                216 GHGKPNTNKSEKAERKSHDTQTTQEICEECEE 247
                                                                                                                                                                                                                                                                                                                                               1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT; 1033 AA
                                                                                                                                                                                                                                POTENTIAL.
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                                                                                                STRAIN-MN1;
MEDLINE-20231818; Pubmed-10768973;
                                                                                                                                                                                    Infect. Immun. 68:2783-2790(2000).
EMBL; AF206527; AAF68255.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N. A.
STRAIN-CANTON S;
MEDLINE-92164624; PubMed-1371458;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000719; Buk_pkinase.
InterPro; IPR003598; Ig_c2.
InterPro; IPR003609; Ig_like.
InterPro; IPR003065; Ig_MHC.
InterPro; IPR001245; Tyr_pkinase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00047; ig; 5.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
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                                                                                                                                                                                                                                                                                                     Local Similarity 56.2 es 18; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1996 (TrEMBLrel. 01-NOV-1996 (TrEMBLrel.
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OTK OR DTRK OR CG8967
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275
275 AA;
                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WCBI_TaxID-7227;
                           Babesia microti.
                                                         NCBI_TaxID=5868;
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SEQUENCE
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.E.,
RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA Gorge R.A. Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Bardon R.C., Rogers Y.-H.C., Blazej K.G., Champe M., Pfeiffer B.D.,
RA Abril J.E., Agbayan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Basud M.R., Bouck J., Brokstein P., Brottier P.,
RA Deckova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F. Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Hostman M.,
Ralush F., Ratpen G.H., Ke Z., Kanison J.A., Recthum K.A.,
Jalali M., Kalush F., Rapen G.H., Ke Z., Kanison J.A., Retteil B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Minnel B.E., Kodirac C.D., Kraft C., Kratt E., Mort S.M., Nixon K., Nusskern D.R., Pacleb J.M.,
Rabor D., Lei Y., Levitsky A.A., Li J., Li J., Liang Y., Lin X.,
Rule B.C., Siden-Klamos I., Simpson M., Strong R., Sun E.,
Shue B.C., Siden-Klamos I., Simpson M., Strong R., Sun E.,
Shue B.C., Siden-Klamos I., Simpson M., Strong R., Sun E.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Walliams S.M., Woodage T., Worley K., Zhan M., Zang S., Pan S., Pollos R.A., Wood R., Shore P.C., Stapler E., Shore P.C., Stapler E., Shore P.C., Stapler E., Shore P.C., Stapler E., Shore P.C., Stapler 
                                                                                                                                                                                                                                                                                                                                                                                                                    Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                          Indels
                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                       11;
                                                                                                                                                                                                                                   PRT; 1033 AA
                   Pred. No. 24;
3; Mismatches
35.6%; Score 38.5; 40.0%; Pred. No. 24
                                                                                                                648 GHSK-SRSKSSGDAQKSDDTACSQQ 671
                                                                                 1 GHXKXNXNKSXXAXXKSXDTQTXQE 25
                                                                                                                                                                                                                                                                           Created)
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MEDLINE-20196006; PubMed-10731132;
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Ig_MHC.
Tyr_pkinase.
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InterPro; IPR003598; Ig_c2.
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Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                           01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2002 (TrEMBLrel. 20,
                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AE003823; AAF58596.1;
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                   Best Local Similarity 40.0
Matches 10; Conservative
                                                                                                                                                                                                                                 PRELIMINARY;
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InterPro; IPR003006;
InterPro; IPR001245;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

July 16, 2003, 17:37:48 ; Search time 7.77066 Seconds Run on:

(without alignments)
848.513 Million cell updates/sec

US-09-853-079-39 Title: Perfect score:

Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

671580 seqs, 206047115 residues Searched:

671580 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Maximum Match 100% Listing first 45 summaries Post-processing: Minimum Match 0%

SPTREMBL 21:* Database :

sp_virus:*
sp_vertebrate:*
sp_unclassified:* sp_invertebrate:* sp_bacteriap:* sp_organelle:* sp_phage:* 1: sp_archea:* 2: sp_bacteria:* sp_archeap:* sp_plant:* sp_rodent:* sp_rvirus:* sp_mammal:* sp_mhc:* sp_fung1:* sp_human:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

		Description	Cit with order Alicoo	Obsima babosia mic	024327 drosophila	09v643 drosophila	007532 bacillus su	09f855 vibrio chol	O9ksw6 vibrio chol	091h95 arabidopsis	Q8sz45 drosophila	Q12288 saccharomyc	Q9vby9 drosophila	O8vig4 mus musculu	O9nxa5 homo sapien	Q9h945 homo sapien	Ogaer7 staphylococ	040201 lotus japon
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		DB) L	n N	'n	16	7	16	10	5	m	2	11	4	4	7	10
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11112222222222222222222222222222222222	4 4 4 4 4 4 4 5 5 4 5 5 5 5 5 5 5 5 5 5

### ALIGNMENTS

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MEDLINE=2021818; PubMed=10768973; Medamath R., Reynolds L.D., Lodes M.J., Houghton R.L., Bruinsma E.S., Mohamath R., Reynolds L.D., Benson D.R., Krause P.J., Reed S.G., Persing D.H.; "Serological expression cloning of novel immunoreactive antigens of Babeata microti."
                                                                                                                             Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Babesiidae; Babesia.
NCBI_TaxID=5868;
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0
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                                                                                                                                                                                                                                                                                                                                                   SEQUENCE 396 AA; 44720 MW; 706E153BA5EE6B7C CRC64;
                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GHXKXNXNKSXXAXXKSXDTQTXQEXXXXXEE 32
                             396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 AA.
                                                           01-0CT-2000 (TrEMBLrel. 15, created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence
01-0CT-2000 (TrEMBLrel. 15, Last annotatiserocactive antigen BMN1-17 (Fragment).
                             PRT;
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EMBL; AF206526; AAF68253.1; -
NON_TER 396 396
                             PRELIMINARY;
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                                                                                                                            Babesia microti
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Q9NIM2;
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Q9NIM2
RESULT 1
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254 FYYDNTVNDIKKNFDESKSKALVLRDKITKKDGDYNTHFEDMIKELNSAAEEFNKIVDIM 313
                                                                    197 ISS---KYKLLVDEISNKAYGTLEGPAADNFDHFRNIWKSIVLKDMFIYCDLLLQHLIYK 253
                                                                                                                     270 FSDVNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLI 329
                                        210 LSAALFRYKEFDDELFKKANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIEN 269
                                                                                                                                                                                               330 ISDCEKKGIKINRDVISSYKLLLSTITYI------VGAGVEAVTVSV 370
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      161 TKEKNKLKKELEKC-----FPEQY--
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF B.
NUMBER OF SEQUENCES: 79
                                                                                                                                                                                                                                                                                                                  107 PNTVGMSLEQFIKNELYSFSNEIYHTISSQISNSFLIMMSDAIVK------HDNYI--- 156
                                                                                              104 PSEAGWSSERF-GYQLLPYSRRI--VIFNEVCLSYIYKHSVMILERDRVNDGHKDYIEEK 160
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                                                                                                                                     -----LKKEGEGCEQIYNYEEFIEKLRGARSEGNNMFQEALIR-FRNASSEEMVNAASY 209
                                                                                                                                                                                                                                          :|: :|| ||: || : ||
197 ISS---KYKLLVDELSNKAYGTLEGPAADNFDHFRNIWKSIVLKDMFIYCDLLLQHLIYK 253
                                                                                                                                                                                                                                                                                            270 FSDVNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLI 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              210 LSAALFRYKEFDDELFKKANDNFGRDDGYDFDYINTKKELVILASVLDGLDLIMERLIEN 269
                        59; Gaps
                                                                                                                                                                           161 TKEKNKLKKELEKC-----FPEQY----SLMKKEELARIFDNAST----
                                                                                                                                                                                                                                                                                                                                                                                               330 ISDCEKKGIKINRDVISSYKLLLSTITYI-----VGAGVEAVTVSV 370
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                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC COMPACTOR OPERATING SYSTEM: PC-DOS/MS-DOS COFFWARE: Patentin Release #1.0, Version #1.30
    Pred. No. 1.2e-10;
; Mismatches 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . 1.2e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
FILING DATE: 11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08990571 Patent No. 6214971
  ilarity 29.3%; Pr
Conservative 50;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           50;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 20:
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(206) 682-6031
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US-08-990-571-20
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Best Local S
Matches 85
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80 PADVAGVSD--GFFIRGONLGAVGSVNEQPNTVGMSLEQFIKNELYSFSNEIYHTISSQI 137
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                                                                                                                                                                                                                                                                                                                                                                  --LKKEGEGCEQIYNYEEFIEKLRGAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      182 SEGNNMFQEALIR-FRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          241 DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180 ---SLMKKEELARIFDNAST-----ISS---KYKLLVDEISNKAYGTLEGPAADNF 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITXI-- 358
                                                                                                                                                                                                                                               Length 367;
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 4; Length 367;
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
             9.6%; Score 246.5; DB 4;
28.8%; Pred. No. 3.6e-11;
tive 53; Mismatches 113;
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STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9.3%; Score 239.5;
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-APR-1997
                                                                                                                                                                                                                                                                                                                                                              138 SNSFLIMMSDAIVK-----HDNYI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 20, Application US/08845258 Patent No. 6183976
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                          Conservative
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CORRESPONDENCE ADDRESS:
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FILING DATE: 24-APR
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STATE: Washington
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                                                         Best Local Similarity Matches 92; Conserv
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US-08-845-258-20
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                      Query Match
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Patent No. 6451315
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Moughton, Raymond L.
APPLICANT: Moughton, Raymond L.
APPLICANT: Compounds and Merhods For THE DIAGNOSIS TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/723,142A
FILING DATE: 01-OCT-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MAKA, David J.
REGISTRATION NUMBER: 31,392
REGISTRATION NUMBER: 31,392
REGISTRATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Local Similarity 28.8%; Pred. No. 3.6
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CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNE...
TELEPAX: (206) C...
TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
""NGTH: 367 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-723-142A-49
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LENGTH: 367
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Best Local S
Matches 92
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241 DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 SNSFLIMMSDAIVK------HDNYI------LKKEGEGCEQIYNYEEFIEKLRGAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 CLSYIYKHSVMILERDRVNDGHKDYIEEKTKEKNKLKKELEKC------FPEQY---- 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEGNNMFQEALIR-FRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 ---SLMKKEELARIFDNAST-----ISS---KYKLLVDEISNKAYGTLEGPAADNF 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 49, Application US/08723142A
Patent No. 6306396
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 367;
                     OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9.6%; Score 246.5; DB 4;
28.8%; Pred. No. 3.6e-11;
tive 53; Mismatches 113;
                                                                                                                                                                                                                             210121.426C2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   342 ITKVSNVIIPGIKALTLTV 360
                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
    IBM PC compatible
                                                                                                                                                                                                                                                                        (206) 622-4900
(206) 682-6031
                                                                                                              11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                               LENGTH: 367 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Seattle
STATE: Washington
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Best Local Similarity
Matches: 92; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                   FILING DATE: 1
CLASSIFICATION:
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TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS AND TREATMENT OF NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: SEED AND BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       132 CLSYIYKHSVMILERDRVNDGHKDYIEEKTKEKNKLKKELEKC------FPEQY---- 179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 SNSFLIMMSDAIVK-----HDNYI------LKKEGEGCEQIYNYEEFIEKLRGAR 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9.6%; Score 246.5; DB 4;
28.8%; Pred. No. 3.6e-11;
tive 53; Mismatches 113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                      FILING DATE: 24-APR-1997
CLASSIF'CGATION: 435
ATTORNEY, FAGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION:
                                                                                                                                                                                 .смыЕR: US/08/845,258
24-APR-1997
N: 127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : |::|::|
342 ITKVSNVIIPGIKALTLTV 360
                                                                                                              IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 49
                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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Best Local Similarity 28.00.
Thes 92; Conservative
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Washington
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                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seattle
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COUNTRY: US
ZIP: 98104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-08-845-258-49
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CITY: Se
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447 EGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN 503
                                                                                     DLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGT
                                                                   387 GTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          334 EKKGIKINNDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               274 NNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 STLTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHODS FOR THE DIAGNOS: OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Mcnelll, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1143; DB 4;
Pred. No. 2.7e-79;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/528,784A CURRENT FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQ ID NOS: 90 SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 49, Application US/08845258
Patent No. 6183976
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Applicant: Sloath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND MET
TITLE OF INVENTION: AND TREATMENT OF
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                           US-09-528-784A-85; Sequence 85, Application US/09528784A; Patent No. 6451315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 44.68;
99.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.1
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT
ORGANISM: Babesia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-528-784A-85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 666
327
                                526
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                                                                                                                                                                                                                                           DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG 360
                                                                                                                                                                                                                                                                                                               59 DNI-----EDNNLKIYA-KQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGM 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      113 SLEQFIKNELYSFSNEIYHTISSQISNSFLIMMSD-AIVKHDNYILKKEGEGCEQIYNYE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------EFIEKLRGARSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKE 219
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|-----PGSTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALN 525
                                                                                                                                                                                                                                                                                                                                                                 AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAG 419
                                                                                                                                                                                                                                                                                                                                                                                    ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 IDFSKREATDSGSFTDILLGNKVKESLSFIEGLISDIKSHSLKAGVTGGISSSSLF---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 87, Application US/09528784A Patent No. 6451315
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278; Conservative
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APPLICANT: Reed, Steven G.
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US-08-723-142A-21
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US-09-528-784A-21
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APPLICANT: Reed, Steven G.
APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIACNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                 Length 492;
                                                                                                                            Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERTING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                              Score 2130; DB 4;
Pred. No. 7.1e-155;
0; Mismatches 2;
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NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/723,142A FILING DATE: 01-OCT-1996 CLASSIFICATION: 536
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                                                                                              83.0%;
SEQUENCE CHARACTERISTICS:
LENGTH: 492 amino acids
TYPE: amino acid
STRANDEDNESS:
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CORRESPONDENCE ADDRESS:
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                                                                                                             Similarity
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                                                      TOPOLOGY:
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Best Local Simi
Matches 417;
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APPLICANT Reed, Michael J.
APPLICANT Houghton, Raymond L.
APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: Moneill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
FILE REFERENCE: 210121.426C4
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
NUMBER OF SEO ID NOS: 90
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83.0%; Score 2130; DB 4;
Best Local Similarity 99.5%; Pred. No. 7.1e-155;
Matches 417; Conservative 0; Mismatches 2;
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}; Pred. No. 7.1e-155;
. 0; Mismatches 2;
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; Sequence 21, Application US/09528784A
; Patent No. 6451315
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99.5%;
TELEPHONE: (206) 622-4900
TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 21.
SEQUENCE CHARACTERISTICS:
                                                                                    LENGTH: 492 amino acids TYPE: amino acid
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Best Local Similarity 99.5 Matches 417, Conservative
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US-08-990-571-21
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                                                                 IEDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGMSLEQFIKN 120
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DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN
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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24 APR-1997
CLASCIPLYAMMENT
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NAME: MAK1, DAVID J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
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TELEFAX: (206)682-6031
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ADDRESSEE: SEED AND
STREET: 6300 Columbia
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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STATE: Washington
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STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                 Score 2130; DB 4;
Pred. No. 7.1e-155;
                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: Reed, Steven G. et
TITLE OF INVENTION: COMPOUNDS
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                               83.0%;
21:
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(206) 682-6031
                                    : LENGTH: 492 amino acids

: TYPE: amino acid

: STRANDEDNESS:

: TOPOLOGY: linear

US-08-845-258-21
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                                                                                                                                                                                  Best Local Similarity 99.5
Matches 417; Conservative
INFORMATION FOR SEQ ID NO:
                     SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 1 CLASSIFICATION:
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181 RSEGNNMFOEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF 240
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                                                                                             Length 503;
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                                                                                             Score 2565; DB 4;
Pred. No. 4.3e-188;
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APPLICANT: Houghton, Raymond L.
APPLICANT: Sleath, Paul R.
APPLICANT: McNeill, Patricia D.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE TITLE OF INVENTION: AND FREATMENT OF B. MICROTI FILE REFERENCE: 210121.42664
CURRENT APPLICATION NUMBER: US/09/528,784A
CURRENT FILING DATE: 2000-03-17
                                                                                             100.0%; Score 2565; 100.0%; Pred. No. 4.
                                                                                                                             0; Mismatches
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NUMBER OF SEQ ID NOS: 90
SCFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 52
LENGTH: 503
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                                              ORGANISM: Babesia Microti
US-08-990-571-52
                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 503; Conservative
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Matches 503; Conserv
                              SOURCE:
             MOLECULE TYPE:
ORIGINAL SOURCE
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                                                             IEDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGMSLEQFIKN 120
                                                                                                                             ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180
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KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
               RSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/990,571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: SEED AND BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    210121.426C2
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FILING DATE: 11-DEC-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 52, Application US/08990571 Patent No. 6214971 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Reed, Steven G. et a TITLE OF INVENTION: COMPOUNDS NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED AND BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (206) 622-4900
TELEFAX: (206)682-6031
INFORMATION FOR SEQ ID NO: 52:
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STATE: Washington
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                                                                                                                                   July 16, 2003, 17:42:54 ; Search time 45.8044 Seconds
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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                  5.1.6
Compugen Ltd
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US-08-990-571-52
US-08-845-258-21
US-08-845-258-21
US-08-920-571-21
US-08-928-784A-21
US-09-528-784A-85
US-08-845-258-49
US-08-845-258-49
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US-08-90-571-20
US-08-90-571-24
US-08-90-571-34
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                  GenCore version
Copyright (c) 1993 - 2003
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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APPLICANT: Lodes, Michael J.
APPLICANT: Houghton, Raymond
APPLICANT: Sleath, Paul R.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE DIAGNOSIS
TITLE OF INVENTION: AND TREATMENT OF B. MICROTI INFECTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 98104
COMPUTER REABABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,258
FILING DATE: 24-APR-1997
CLASSIFICATION: 435
ATTORNET/AGENT INFORMATION:
NAME: Waki, David J.
REGISTRATION NUMBER: 210121.426C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPHONE: (206) 622-631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: SEED AND BERRY 6300 Columbia Center, 701 Fifth Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 2565; DB 4;
100.0%; Pred. No. 4.3e-188;
ive 0; Mismatches 0;
                                                US-08-723-142A-25
US-09-528-784A-25
US-07-609-716-31
US-08-175-155-29
US-08-177-509B-64
US-08-777-237A-35
US-08-77-237A-35
US-08-707-237A-66
US-08-845-258-25
US-08-990-571-25
                                                                                                                                                                                                               US-09-444-791A-64
US-08-175-155-48
                                                                                                                                                                            -08-475-411A-31
-08-478-029A-31
                                                                                                                                                                                                                                                  US-08-707-237A-54
US-08-806-029-10
                                                                                                                                                                                                                                                                                      US-08-477-509B-83
                                                                                                                                                                                                                                                                                                                                           ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 52, Application US/08845258 Patent No. 6183976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BERRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Babesia Microti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 503 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 503; Conservative
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463
11177
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11059
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM:
US-08-845-258-52
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Sequence

US-08-482-085B-94 US-09-444-791A-94

1038 1011 1011 1011

Sequence Sequence

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12;
                                                                                                                                            80 PADVAGVSD--GFFIRGQNLGAVGSVNEQPNTVGMSLEQFIKNELYSFSNEIYHTISSQI 137
                                                                                                                                                                                                                              182 SEGNNMFQEALIR-FRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF 240
                                                                                                                                                                  241 DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
                                                                                                                                                                                                          138 SNSFLIMMSDAIVK------HDNYI-----LKKEGEGCEQIYNYEEFIEKLRGAR 181
                                                                                                                                                                                                                                                                                               301 DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYI-- 358
                                                                                                                                                                                                                                                                                                                                                                                                                             285 DGDYNTHFEDMIKELNSAAEEFNKIVDIMISNI---GDYDEYDSIASFKPFLSMITEITK 341
                                                                                                                61; Gaps
other tick-borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
                                                                            9.6%; Score 246.5; DB 19; Length 367; 28.8%; Pred. No. 1e-08; tive 53; Mismatches 113; Indels 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         342 ITKVSNVIIPGIKALTLTV 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----VGAGVEAVTVSV 370
                                                                            Query Match
Best Local Similarity 28.88
Matches 92; Conservative
                                                367 AA;
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Search completed: July 16, 2003, 17:46:45 Job time: 141.806 secs us-09-853-079-52.rag

especially useful for enhancing immune response against B. microti. infection. The present sequence was used to illustrate the invention.

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Seguence

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                                                                                                                                                                                                 EKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSAT 393
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                                                                                                                                                                                                                                                              The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are
                                                                                                                                                                          99
coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                  NNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDC
                                                                                                                                                               STLIGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDK
                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  microti infection, and as component of a composition for enhancing immune response against B. microti infections -
                                                                                                                                                                                                                                                                                                             AGTGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN 503
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                                                                                                 Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protozoacide; vaccine; antigen; antigenic epitope; infection.
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                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Babesia microti antigenic epitope fusion protein BaF-5.
                                                                                                  23;
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0
                                                                                                  Score 1143; DB 23
Pred. No. 8.9e-69;
                                                                                                                         2; Mismatches
                                                                                                             Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                    ABB88989 standard; Protein; 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0605724.
2000US-0656688.
2000US-0685436.
2000US-0737178.
2001US-0794764.
                                                                                                  44.68;
99.18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-MAY-2001; 2001WO-US15192
                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                           Conservative
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                                                                                                             Similarity
                                                                          666 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Babesia microti
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07-SEP-2000;
10-OCT-2000;
13-DEC-2000;
26-FEB-2001;
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                                                                           Sequence
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                                                                                                  Query Match
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276 TDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDCEK 335
                                                                                                                                                                                          455
                                                                                                                                                                                                                      570 LTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAG 629
                                                                                                                                                 336 KGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSATST
                                                                                                                                                                                            LTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAG
                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nseq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The sequence is that of a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:
(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and
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             677;
                                                                                                                                                                                                                                                    TGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN 503
                                                                                                                                                                                                                                                                   antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.
               Length
                                           Indels
                                            0
44.5%; Score 1141; DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PR;
                          100.0%; Pred. No. 1.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 94-95; 113pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             infection and in protective vaccines
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                                                                                                                                                                                                                                                                                                                                                          AAW56301 standard; Protein; 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed
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96US-0723142.
                           Best Local Similarity 100.
Matches 228; Conservative
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               Query Match
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09-MAY-2001;
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Example
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                                                                                                                                                                                                                                                                EGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN 503
                                        SMDDIIA----MFSN------PNMYLVKVAYLQAIEHIFLISTKYND----IFDYT
                                                                                            -------EFIEKLRGARSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKE
                                                                                                                           FDDELFKKANDNFGRDDG-----YDFDYINTKK-----ELVILASVLDGLDLIMERL
                                                                                                                                    IENFSDVNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALN
                                                                                                                                                                   DLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGT
                                                                                                                                                                                                  GTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGGTSGTTTSSGAASGKAGTGTAGTTTSS
                                                                                                                                                                                                                                SLEQFIKNELYSFSNEIYHTISSQISNSFLIMMSD-AIVKHDNYILKKEGEGCEQIYNYE
                              DNI-----EDNNLKIYA-KQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGM
                                                                                                           IDFSKREATDSGSFTDILLGNKVKESLSFIEGLISDIKSHSLKAGVTGGISSSSLF
Length 1132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD;
                                                                                                                                                                                                                                                                                                                                                                         parasite; tick-borne illness; antigen; disease prevention.
               Indels
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                                                                                                                                                                                                                                                                                                                                                              B. microti MN-10/BMNI-17 fusion protein SEQ ID NO: 85
23;
               .68
45.2%; Score 1159.5; DB 58.3%; Pred. No. 1.4e-69;
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               35; Mismatches
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                                                                                                                                                                                                                                                                                                                Protein;
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17-MAR-2000; 2000US-0528784.
                Conservative
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                                                                                                                                                                                                                                                                                                                AAB30230 standard;
                                                                                                                                                                                                                                                                                                                                                                               rodent
                                                                                                                                                                                                                                                                                                                                                                                      disease diagnosis;
        Similarity
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        Local Simi
hes 278;
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their
                            The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  393
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                                                                                                                                                                                                                                                                                                           EKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGTGTSVSAT
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                                                                                                                                                                                                                                                                                      274 NNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALNDLIISDC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to novel Babesia microti antigens and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and treating B. n for enhancing
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AGTGTSGTTTSSGTCAGGAGSGGPSGHASNAKIPCIMTLTLFALLTFIVN 503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protozoacide; vaccine; antigen; antigenic epitope; infection.
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PD,
                                                                                                                                                                                                              Length
                                                                                                                                                                                                                                                   Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BaF-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful for diagnosing a conent of a composition
                                                                                                                                                                                                              21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          protein
                                                                                                                                                                                                            Score 1143; DB 21;
Pred. No. 8.9e-69;
2; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New Babesia microti antigens, useful for diagramicroti infection, and as component of a component ersponse against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Babesia microti antigenic epitope fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ä.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         999
7; Page 108-111; 118pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000US-0605724.
2000US-0656688.
2000US-0685436.
2000US-0737178.
2001US-0794764.
                                                                                                                                                                                                              44.6%;
99.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein;
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                                                                                                                                                                                                                                   Best Local Similarity 99.1
Matches 228; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-216691/27
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                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                          666 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Babesia microti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200185947-A2
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10-OCT-2000;
13-DEC-2000;
26-FEB-2001;
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ThuvJul

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(CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                  Babesia microti
                                                                                                                                                                                                                                                                                                                                                       Babesia microti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1132
                                                                                                                                                                                                                                                                                                                                                                         WO200185947-A2.
                                                                                                                                                                                                                                                                                                                                                                                                              09-MAY-2001;
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13-DEC-2000;
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07-SEP-2000;
                                                                                                                                                                                                                                                                                             20-JUN-2002
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           369
                              220
                                                 425
                                                                                      472
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                                                                                                                             526
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                                       360
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DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMDDIIA----MFSN------PNMYLVKVAXLQAIEHIFLISTKYND----IFDYT 368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --------EFIEKLRGARSEGNNMFQEALIRFRNASSEEMVNAASYLSAALFRYKE 219
                                                                            AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAG 419
                                                                                     New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective
           DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG
                                                 SLEQFIKNELYSFSNEIYHTISSQISNSFLIMMSD-AIVKHDNYILKKEGEGCEQIYNYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59 DNI-----EDNNLKIYA-KQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 1132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75;
                                                                                                                                                                                                      B. microti MN-10/BMNI-17/BMNI-15 fusion protein SEQ ID NO:
                                                                                                                                                                                                                       parasite; tick-borne illness; antigen; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                            McNeill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1159.5; DB Pred. No. 1.4e-69;
                                                                                                                                                                                                                                                                                                                                                                                           Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 7; Page 112-116; 118pp; English
                                                                                                                                             AAB30231 standard; Protein; 1132 AA
                                                                                                                                                                                                                                                                                                                                                                                            Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35;
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                                                                                                                                                                                                                                                                                                                       05-APR-2000; 2000WO-US09136
                                                                                                                                                                                                                                                                                                                                           05-APR-1999; 99US-0286488
17-MAR-2000; 2000US-0528784
                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         278; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             a patient
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                                                                                                                                                                                                                                                                                                                                                                        (CORI-) CORIXA CORP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1132 AA;
                                                                                                                                                                                                                          Babesiosis; rodent
                                                                                                                                                                                                                                    disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                 WO200060090-A1.
                                                                                                                                                                                                                                                                                                                                           05-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                        antigen and I treating or I immunity in a
                                                                                                                                                                                    12-FEB-2001
                                                                                                                                                                                                                                                                                                    12-OCT-2000
                                                                                                                                                                                                                                                       Babesia sp.
                                                                                                                                                                                                                                                                 Synthetic.
                                     301
                                                       373
                                                                           361
                                                                                             433
                                                                                                                                                                 AAB30231;
                                                                                                                                                                                                                                                                                                                                                                                          Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               --YDFDYINTKK----ELVILASVLDGLDLIMERL
                                                                                                            267 IENFSDVNNTDDIKKAFDECKSNAIILKKKILDNDEDYKINFREMVNEVTCANTKFEALN
                                                                                                                                                                                                              DLIISDCEKKGIKINRDVISSYKLLLSTITYIVGAGVEAVTVSVSATSNGTESGGAGSGT
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EGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGHASNAKIPGIMTLTLFALLTFIVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB88976 standard; Protein; 1132
                                                                            FDDELFKKANDNFGRDDG----
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2000US-0656688.
2000US-0685436.
2000US-0737178.
2001US-0794764.
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73 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180
   433 AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTWFG 491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEYEHTELAKEHCKKEKCVNVDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IEDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGMSLEQFIKN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention relates to novel Babesia microti antigens and to coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 492;
                                                                                                                                                                                                  Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McNe111
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Pred. No. 1.9e-135;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RL, Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Page 78-79; 195pp; English
                                                                              Ā
                                                                           ABB88937 standard; Protein; 492
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0
                                                                                                                                                                     Babesia microti antigen BMNI-4.
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2000US-065688.
2000US-0685436.
2000US-0737178.
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99.5%;
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Best Local Similarity 99.5
Matches 417; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-216691/27.
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                                                                                                                                                                                                                                                            W0200185947-A2.
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07-SEP-2000;
10-OCT-2000;
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26-FEB-2001;
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                                                                                                         ABB88937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Secrist
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
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                                                                                                                                                                                                                                                                                                                                                                                                               New polypeptides containing an antigenic portion of Babesia microti antityen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
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                                                                                          tick-borne illness; antigen;
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                                                                                                                                                                                                                                                                                                                                     McNeill
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Pred. No. 1.9e-135;
); Mismatches 2;
                                                                                                                                                                                                                                                                                                                                     Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 72-73; 118pp; English
                                                                                        parasite; tick-born disease prevention.
                                                            microti BMNI-4 antigen SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                     RL,
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99.5%;
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17-MAR-2000; 2000US-0528784.
                                                                                                                                                                                                                             05-APR-2000; 2000WO-US09136
                                 (first entry)
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                                                                                                                                                                                                                                                                                                       (CORI-) CORIXA CORP
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N-PSDB; AAC65081.
                                                                                          rodent
                                                                                                        disease diagnosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              492 AA;
                                                                                                                                    Babesia microti.
                                                                                                                                                                  WO200060090-A1.
                               12-FEB-2001
                                                                                          Babesiosis;
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AAB30191;
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Homer MJ;

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Babesia microti; antigen; immunogen; diagnosis; infection; vaccine; immunity; detection.
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                                                                                                                           97US-0990571.
                                                                                                                                                                                                                                                                                                                                                                                                                      Best_Local Similarity 99.5
Matches 417; Conservative
                                                                                                                                                                                 Houghton R,
                                                                                                                                                             MAYO-) MAYO FOUNDATION
                                                                                                                                                                                                                 WPI; 1999-385612/32
                                                                                                                                                                                                                                                                                                                                                                                     492 AA;
                                                                                                                                                                                                                             N-PSDB; AAX88998
                                                                                                                                                 CORI-) CORIXA
                                                                                                     11-DEC-1998;
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                                                         WO9929869-A1
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                                                                               17-JUN-1999
                                                                                                                                                                                            Sleath PR;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
                                                                                                                                                                   The sequence is that of a polypeptide comprising at least one antigent portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:

(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lymme disease and ehrlichiosis) that have similar symptoms but require different treatments.
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                                                                                                                                                                                                                                                                                                                                         Length 492;
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                                                                                                                                                                                                                                                                                                                                       Score 2130; DB 19;
Pred. No. 1.9e-135;
0; Mismatches 2;
                                  Sleath PR;
                                                                                                                           infection and in protective vaccines
                                                                                                                                              Claim 1; Page 49-51; 113pp; English.
                                  Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Babesia microti antigen BMNI-4.
                                                                                                                                                                                                                                                                                                                                        83.0%;
99.5%;
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                                  Lodes MJ,
            (CORI-) CORIXA CORP.
                                                       1998-195465/18
                                                                                                                                                                                                                                                                                                                                                  Local Similarity es 417; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY24342 standard;
                                                                                                                                                                                                                                                                                                                  492 AA;
                                                                  N-PSDB; AAV22734
                                  Houghton R,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        specific immunogenic portions of Babesia microti. AAX88933 to AAX88999 encode specifically claimed B. microti immunogenic proteins, and AAX2437 to AAX4338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. They microti infections. The present sequence represents a B.microti antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEYEHTELAKEHCKKEKCVNVDN
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                                                                                                                                                                                                                                              present invention describes isolated polypeptides comprising
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 492;
  Reed
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à
  Persing
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                                                                                                                                                  New isolated Babesia microti polypeptides
                                                                                                                                                                                                Example 1; Page 72-74; 126pp; English.
Lodes MJ,
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121 ELYSPENBITWITSSO(SMSFLIMMSDNITMENDRYLLAKEDECCECTETATION   10   11   11   11   11   11   11   1	Qy Dp	61 IEDNNLKITAKQFKSVYTPPADVAGVSDGFFIRGONLGAVGSVNEQPNTVGMSLEQFIKN 120	ខ្លួន	The present invent coding sequences.
131 ELYSENSHIPPELTERANSESEROWANGURALINENSETERALS 100  152 ELYSENSHIPPELTERANSESEROWANGURALINENSETERANDOR 200  153 ELYSENSHIPPELTERANSESEROWANGURALINENSETERANDOR 200  154 ELYSENSHIPPELTERANSESEROWANGURALINENSETERANDOR 200  155 ENGINEER 201  156 ELYSENSHIPPELTERANSESEROWANGURALINENSETERANDOR 200  157 ELYSENSHIPPELTERANSESEROWANGURALINENSETERANDOR 200  158 ENGINEER 201  150 ENGINEER 201  15	ò	ELYSFSNEIYHTISSOISNSFLIMMSDAIVKHDNYII.KKEGEGCEOTVNYEEFIEKIEGE	S.	diagnosing and tre
181 RSEGNAMPOLISHERNASSERONAAATTSAALFFKTETOELFKKANDWFCEDCTUF 240   SOG SEQUENCE   SOG SECUENCE	. <u>8</u>		80 <b>%</b>	infection. The
13	à	RSEGNNMFOEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF	ÖS	
241 DYTRYKEEVILASVILGEDLINSKILDRYKENNONTKAKPERSONANTIAKKTILDN 300 0 0 1 1 2 41 DYTRYKEEVILASVILGEDLINSKILDRYBONKENNONTKAKPEKSANILIAKKTILDN 300 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	op q		<b>ĕ</b>	ery Match
241 DYTHYREELYILASYLOGIDIANSKILINNESDAWANDERKRILLAKKILINN 300 DD 44 301 DEDTYCHYREELYILASYLOGIDIANSKILINNESDAWANDERKRILLAKKILINN 300 DD 64 302 DEDTYCHYRERANGERGAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	ά	DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN	W	445
301 DEDYKINERPONNEYCKOKTGYKTGYKTGYKTGYTGYTGYG 366 301 DEDYKINERPONNEYCKOANTEFRALMDIISCEKGKTGKINENDISSYLLLGYTTTTGG 366 301 DEDYKINERPONNEYCKOANTEFRALMDIISCEKGKTGKINENDISSYLLLGYTTTTGG 366 301 DEDYKINERPONNEYCKOANTEFRALMDIISCEKGKTGKINENDISSYLLLGYTTTTGG 366 301 DEDYKINERPONNEYCKOANTEFRALMDIISCEKGKTGKINENDISSYLLLGYTTTTGG 367 421 TSCTTTSSCEAGGGKGTGTTGTTTTSSCEAGGGKGTGTTTSSCTGGGGGGGGG 420 421 TSCTTTSSCEAGGGKGTGTTATTTSSCEAGGGKGTGTTTSSCTGGGGGGGGGGGGGGGGGGGGGGGGGG	ą	DYINTKKELVILASVLDGLDLIMERLIENFSDVNNTDDIKKAFDECKSNAIILKKKILDN	Š Š	
301 DEDYKINFRAMONEVCANTREALMELISDEEKKGIKINENDISSYKLÄLÄSTITTIG 360 361 AGVEAVVOSSYRSGEGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	λ	DEDYKINFREMVNEVTCANTKFEALNDLIISDCEKKGIKINRDVISSYKLLLSTITYIVG	ara Ao	
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421 TSGTTTSSCAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGH 480  421 TSGTTTSSCAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGH 480  421 TSGTTTSSCAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGGAGGCSGGPSGH 480  481 ASNAKIPGINFLILFALIPPIVN 503  48899024  481 ASNAKIPGINFLILFALIPPIVN 503  482 ASNAFORD 500 CONTACT SALE AND	<b>₹</b> 6	AGVEAVIVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGG	70 V	
481 ASNAKIPGINITHINITHINITHINITHINITHINITHINITHINIT	á	TSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGGGGGG	q _O	
481 ASNAKIPGIMULITARALITERINW 503  481 ASNAWSO24  482 Babesia microti antigen MN-10 variant.  Protozoacider vaccine; antigen; antigenic epitope; infection.  Protozoacider vaccine; antigen mN-10 variant.  Protozoacider vaccine; antigen antigenic epitope; infection.  DD 393  Babesia microti.  WOZOO185947-A2.  15-NOV-2001.  10-MAY-2001; 2001W0-0815192.  10-MAY-2001; 2001W0-0815192.  11-NOV-2001  10-MAY-2001; 2001W0-0815192.  11-NOV-2001  11-NOV	. g		60 4	
481 ASNAKIPGINTITLFALITFINA 503  189024 ADB89024 standard; Protein; 452 AA. ADB89024 standard; Protein; 452 AA. ADB89024 standard; Protein; 452 AA. ADB89024: DO-JUN-2002 (first entry) Babesia microti antigen mN-10 variant. Protozoacide; vaccine; antigen; epitope; infection. DD 393 Babesia microti. WO200185947-A2. 15-NOV-2001. 15-NOV-2001. 10-MAY-2002. 200008-056374 10-MAY-2003. 200008-056374 10-MAY-2003. 200008-056374 10-MAY-2003. 200008-056346 10-MAY-2003. 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 20008-056346 2	ζĊ	ASNAKIPGIMTLTLFALLTFIVN	2 6	
99 301  89024 standard; Protein; 452 AA.  ABB89024 standard; Protein; 452 AA.  ABB89024:  20-JUN-2002 (first entry)  Babesia microti antigen MN-10 variant.  Protozoacide; vaccine; antigenic epitope; infection.  Babesia microti.  WO200185947-A2.  15-NOV-2001.  10-MX-2001; 2001W0-USIS192.  10-MX-2001; 2001W0-USIS192.  10-MX-2001; 2001W0-USIS192.  11-NOV-2001.  12-NOV-2001.  13-NOV-2001.  13-NOV-2001.  1481  10-MX-2001; 2001W0-USIS192.  10-MX-2001; 2001W0-USIS193.  11-NOV-2001.  12-NOV-2001.  13-NOV-2001.  13-NOV-2001.  1481  15-NOV-2001.  15-NOV-2001.  16-NOV-2001.  17-NOV-2001.  18-NOV-2001.  20-NOV-2001.  20-NO	q	ASNAKIPGIMTLTLFALLTFIVN	යි අධ	
ABB89024 standard; Protein, 452 AA.  ABB89024 standard; Protein, 452 AA.  ABB89024;  20-JUN-2002 (first entry)  Babesia microti antigen MN-10 variant.  Protozoacide; vaccine; antigen; antigenic epitope; infection.  Protozoacide; vaccine; antigen; antigenic epitope; infection.  Drotozoacide; vaccine; antigen MN-10 variant.  Protozoacide; vaccine; antigen; antigenic epitope; infection.  Drotozoacide; vaccine; antigen; antigenic epitope; infection.  Drotozoacide; vaccine; antigen; antigenic epitope; infection.  Drotozoacide; vaccine; antigen; antigenic epitope; infections  Drotozoacide; vaccine; antigen; antigenic epitope; infections  Drotozoacide; vaccine; antigenic epitope; and treating B.  Drotozoacide; vaccine; antigenic epitope; and as composition for enhancing  Drotozoacide; vaccine; antigenic epitope; and as composition for enhancing  Drotozoacide; vaccine; antigenic epitope; and as composition for enhancing  Drotozoacide; vaccine; antigenic epitope; and as composition for enhancing  Drotozoacide; vaccine; antigenic epitope; and as composition for enhancing  Drotozoacide; vaccine; antigenic epitope; and as composition for enhancing  Drotozoacide; vaccine; antigenic epitope; and as composition for enhancing  Drotozoacide; vaccine; antigenic epitope; and as composition for enhancing  Drotozoacide; vaccine; antigenic epitope; and as composition for enhancing  Drotozoacide; antigenic epitope; and as composition for enhancing  Drot	RESUL	in the second se	QY	
ABB89024; 20 -JUN-2002 (first entry) Babesia microti antigen MN-10 variant. Protozoacide; vaccine; antigen; antigenic epitope; infection. Protozoacide; vaccine; antigen; antigenic epitope; infection. Protozoacide; vaccine; antigen; antigenic epitope; infection.  Drotozoacide; vaccine; antigen; antigenic epitope; infections and as component of a composition for enhancing and treating B. Mr. 1200-1105  Drotozoacide; vaccine; antigen; antigenic antigeni	ID OI	89024 standard; Protein; 452	qa	
20-JUN-2002 (first entry)  Babesia microti antigen MN-10 variant.  Protozoacide; vaccine; antigen; antigenic epitope; infection.  Protozoacide; vaccine; antigen; antigenic epitope; infection.  Babesia microti.  WO200185947-A2.  15-NOV-2001.  10-NAY-2001.  10-NAY-2001.	ž ų	ABB89024;	QY	
Protezoacide; vaccine; antigen NN-10 variant.   Drotection.   Drotecti	ž fi č	(first	qa	1111 364 AGVE
Protozoacide; vaccine; antigen; antigenic epitope; infection.   Db   393	<u> </u>	microti antigen MN-10	δŏ	
### Babesia microti.  ### W0200185947-A2.  ### W020018506938.  ### W020018506938.  ### W020018506938.  ### W020018506934.  ### W020018506	5 € ₹	antigen; antigenic epitope;	qa	393
## W0200185947-A2.  ## W0200185947-A2.  ## B W0200185947-A2.  ## B W020018	585	Babesia microti.	Qy	
15-NOV-2001.  10-MAY-2001; 2001WO-US15192.  10-MAY-2000; 2000US-0569098.  10-MAY-2000; 2000US-0569098.  10-OCT-2000; 2000US-0565688.  10-OCT-2000; 2000US-0565688.  11-DEC-2000; 2000US-0685436.  12-DEC-2000; 2000US-0685436.  13-DEC-2000; 2000US-0685436.  14-DEC-2000; 2000US-0685436.  15-DEC-2000; 2000US-0685436.  15-DEC-2000; 2000US-0685436.  16-DEC-2000; 2000US-0685436.  17-DEC-2000; 2000US-0685436.  18-DEC-2000; 200US-0685436.  18-DEC-2000; 200US-06854.  18-DEC-2000; 200US-0685436.  18	5 Z S	WO200185947-A2.	qu	433 ASNA
09-MAY-2001; 2001W0-US15192.  10-MAY-2000; 2000US-0569088.  27-JUN-2000; 2000US-0565688	<b>5</b> €	15-NOV-2001.		
10-MAY-2000; 2000US-0569098.  27-JUN-2000; 2000US-065688.  27-JUN-2000; 2000US-065688.  10-O-SEP-2000; 2000US-065688.  11-DEC-2000; 2000US-065688.  12-DEC-2000; 2000US-063688.  13-DEC-2000; 2000US-0737178.  26-FEB-2001; 2001US-0794764.  CORI-) CORIXA CORP.  Read SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD, Homer MJ; NX X antigen; NY different Secrist H; NX X NY EP834567-  New Babesia microti antigens, useful for diagnosing and treating B. NX X NY New Babesia microti infection, and as component of a composition for enhancing PP NX NY NY NAPR-19 NAP	5 E S		AAW	000
13-DEC-2000; 20000S-0686386.   DY X		10-MAX-2000; 2000US-0569098. 2-5-5-00-2000; 2000US-0569724.	YX P	
KW Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD, Homer MJ; Secrist H; WPI: 2002-216691/27.  New Babesia microti antigens, useful for diagnosing and treating B. Microti infection, and as component of a composition for enhancing immune response against B. microti infections - Immune response against B. microti infections - Immune response Against B. PR  XX Claim 2; Page 188-190; 195pp; English.		10-OCT-2000; 2000US-0685436. 13-DEC-2000; 2000US-0731178. 26-FEB-2001; 2001US-0794764.	X D X E	28-SEP-1998 Babesia micro
Reed SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD, Homer MJ; XX Secrist H;  NET: 2002-216691/27.  New Babesia microti antigens, useful for diagnosing and treating B.  Microti infection, and as component of a composition for enhancing  Mimune response against B. microti infections .  XX Claim 2; Page 188-190; 195pp; English.		(CORI-) CORIXA CORP.	XX KW	antigen; dete
WPI; 2002-216691/27.  New Babesia microti antigens, useful for diagnosing and treating B.  microti infection, and as component of a composition for enhancing  immune response against B. microti infections -  Claim 2; Page 188-190; 195pp; English.	X II II I	SG, Lodes MJ, Houghton RL, Sleath PR, McNeill PD, Homer 1st H;	XXX	differentiati Babesia micro
New Babesia microti antigens, useful for diagnosing and treating B.  Microti infection, and as component of a composition for enhancing  immune response against B. microti infections -  Claim 2; Page 188-190; 195pp; English.	X Z X	WPI; 2002-216691/27.	X A	EP834567-A2.
XX Claim 2; Page 188-190; 195pp; English. PR PR PR		New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections	XX PF	08-APR-1998. 01-OCT-1997;
	× S ×	Claim 2; Page 188-190; 195pp; English.	XX PR	24-APR-1997; 01-0CT-1996:

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POEALIRFRNASSEEMVNAASYLSAALFRYKEFDDELFKKANDNFGRDDGYDF 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ntion relates to novel Babesia microti antigens and their. The B. microti antigens, antigenic epitopes of such mpositions comprising such antigens are useful for reating B. microti infection. The compositions are if for enhancing immune response against B. microti resent sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                     YAKQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGMSLEQFIKN 120
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                                                                                                                                                                                                                                                                                  MNGIHYYYIDGSLLASGEVTSNFRYISKEYEFHTELAKEHCKKEKCVNVDN 60
                                                                                                                                                                                                                                                                                                             51; Gaps
                                                                                                                                                                                             87.3%; Score 2239.5; DB 23; Length 452;

y 89.0%; Pred. No. 7.3e-143;

ervative 0; Mismatches 4; Indels 51;
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60S-0723142.
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420 420 480 480

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1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEYEHTELAKEHCKKEKCVNVDN 60
                                                   421 TSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGH
                                       AGVEAVTVSVSATSNGTESGGAGSGTGTSVSATSTLTGNGGTESGGTAGTTTSSGTEAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention relates to novel Babesia microti antigens and to coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homer MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
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                                                                                                                                                                                                                                                                                                                                             Protozoacide; vaccine; antigen; antigenic epitope; infection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 14; Page 102-103; 195pp; English.
                                                                                                                                                          481 ASNAKIPGIMTLTLFALLTFIVN 503
                                                                                                                                                                                                                                       AA.
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                                                                                                                                                                                                                                       ABB88961 standard; Protein; 503
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2000US-0656688.
2000US-0685436.
2000US-0737178.
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10-OCT-2000;
13-DEC-2000;
26-FEB-2001;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IEDNNLKIYAKQFKSVVTTPADVAGVSDGFFIRGQNLGAVGSVNEQPNTVGMSLEQFIKN 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
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                                                                                                                                                         parasite; tick-borne illness; antigen;
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100.0%; Pred. No. 9.8e-165;
ive 0; Mismatches 0;
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                                                                                                                               52
                                                                                                                                                                       disease prevention.
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                                                                                                                              B. microti clone antigen SEQ ID NO:
                                                AAB30216 standard; Protein; 503 AA.
                                                                                                                                                                                                                                                                                                                                                                     Houghton RL,
                                                                                                                                                                                                                                                                          05-APR-2000; 2000WO-US09136
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17-MAR-2000; 2000US-0528784
                                                                                                     (first entry)
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Best Local Similarity 100.
Matches 503; Conservative
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                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
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                                                                                                                                                        Babesiosis; rodent
                                                                                                                                                                       disease diagnosis;
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17-JUN-1999

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Babesia

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                                                                                                                                                                                                                                                                          Babesia microti antigen MN-10 complementary open reading frame protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    TSGTTTSSGAASGKAGTGTAGTTTSSEGAGSDKAGTGTSGTTTSSGTGAGGAGSGGPSGH
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                                                                                                                                                                                                                                                               1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
                                                                                                                                                                                                                                                                                                                                                   ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA
                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunogen; diagnosis; infection; vaccine;
                                                             one antigenic portion of a Balesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection by detecting specific antibodies in usual immunoassays. Infection by detecting sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
antibodies, useful for diagnosis of
                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                  100.0%; Score 2565; DB 19; Length 503; llarity 100.0%; Pred. No. 9.8e-165;. Conservative 0; Mismatches 0; Indels 0;
                                                     sequence is that of a polypeptide comprising at least
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English
vectors, transformed cells and antib
Infection and in protective vaccines
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; Protein; 503
                               Claim 1; Page 99-101; 113pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                            Local Similarity
es 503; Conserv
                                                                                                                                                                                              503 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ELYSFSNEIYHTISSQISNSFLIMMSDAIVKHDNYILKKEGEGCEQIYNYEEFIEKLRGA 180
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                                                                                                                                                   The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88983 to AAX88994 encode. specifically claimed B. microti immunogenic proteins, and AAY24315 to AAY24338 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B. microti infections. The present sequence represents a B.microti antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 KRFNEHTDMNGIHYYYIDGSLLASGEVTSNFRYISKEYEYEHTELAKEHCKKEKCVNVDN
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Persing D,
                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                             New isolated Babesia microti polypeptides
                                                                                                                           Example 1; Page 107-108; 126pp; English.
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   Houghton
                                               WPI; 1999-385612/32.
N-PSDB; AAX90016.
                                                                                                                                                                                                                                                                                                                              Local Similarity
Les 503; Conserv
                                                                                                                                                                                                                                                                                    503 AA;
   Bruinsma E,
                Sleath PR;
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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model
SW
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1
protein
Σ

July 16, 2003, 17:36:24; Search time 140.806 Seconds Run on:

(without alignments)
476.010 Million cell updates/sec

2565 1 KRENEHTDMNGIHYYYIDGS......AKIPGIMTLTLFALLTFIVN 503 US-09-853-079-52 Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

908470 segs, 133250620 residues Searched:

908470 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

/ SIDS2/gcgdata/geneseq/geneseqp-embl/AA1989.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1991.DAT:*/SIDS2/gcgdata/a/neneca/ /SIDS2/gcgdata/geneseg/genesegp-emb1/AA1994.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:* /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:
/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1985.DAT:
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1988.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980.DAT: /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT: /gcgdata/geneseg/genesegp-embl/AA2001.DAT; /gcgdata/geneseq/geneseqp-embl/AA1993. /SIDS2/gcgdata/geneseg/genesegp-embl/AA2000./SIDS2/gcgdata/geneseg/genesegp-embl/AA2001. /SIDS2/gcgdata/geneseq/geneseqp-embl/AA1998 /SIDS2/gcgdata/geneseq/genesegp-embl/AA1992 IDS2/gcgdata/geneseq/geneseqp-embl/AA1995 /SIDS2/gcgdata/geneseq/genesegp-embl/AA1996 /gcgdata/geneseq/geneseqp-embl/AA1997 /SIDS2/gcgdata/geneseg/genesegp-embl/AA1999 A_Geneseq_101002: /SIDS2

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

		oР				
Result		Query				
NO.	Score	Match	Match Length DB ID	DB	ID	Description
н	2565	100.0		19	AAW56302	Babesia microfi MN
~	2565	100.0		20	AAY24364	Babesia microti an
e	2565	100.0		21	AAB30216	B. microti clone a
4	2565	100.0		23	ABB88961	Babesia microti an
5	2239.5	87.3		23	ABB89024	Babasia micrott an
9	2130	83.0		19	AAW56281	Rabesia microfi BM
7	2130	83.0		20	AAY24342	Babesia microti an
8	2130	83.0	492	21	AAB30191	B. microti BMNI-4
6	2130	83.0		23	ABB88937	Babesia microti an
10	1159.5	45.2	-	21	AAB30231	B. microti MN-10/B

Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid,

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WPI; 1998-195465/18. N-PSDB; AAV22748.

abesia microti microti MN-10 abesia microti abesia microti abesia microti abesia microti	B. microti BNNI-3 Babesia microti an Babesia microti an Babesia microti an Babesia microti an B. microti BNNI-3 B. microti BNNI-3 Babesia microti an	microti microti microti microti	BMNI- BMNI- croti croti PER C PER A	Repetitive protein FCB-SLP protein fr SELPF amino acid s SELPF synthetic pr Amino acid sequenc 158PlD7 SSH nuclei Babesia microti BM Babesia microti an B. microti BMI-10
ABB8897 AAB3023 ABB8897 ABB8898 AAW5630 AAY2436	AAB30215 ABB88960 ABB04680 AAW56279 AAX24341 AAR30190			
				1038 22 1038 22 1011 21 1170 19 231 23 463 19 463 20
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11 12 13 14 15	18 18 20 23 23	. 255 26 27 28 29	3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3	3387 444444 2432 2433 2433 2433

## ALIGNMENTS

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antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.
                                                                                                                                                                                                            Sleath PR;
                                                              Babesia microti MN-10 antigen sequence.
              AAW56302 standard; Protein; 503 AA.
                                                                                                                                                                                                            Reed SG,
                                                                                                                                                     97EP-0117067.
                                                                                                                                                                    97US-0845258
96US-0723142
                                               (first entry)
                                                                                                                                                                                                            Lodes MJ,
                                                                                                                                                                                           (CORI-) CORIXA CORP.
                                                                                                     Babesia microti
                                                                                                                                                     01-OCT-1997;
                                                                                                                                                                    24-APR-1997;
01-OCT-1996;
                                                                                                                                                                                                           Houghton R,
                                              28-SEP-1998
                                                                                                                     EP834567-A2
                                                                                                                                     08-APR-1998
                               AAW56302;
RESULT 1
        AAW56302
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Sequence
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                                                                                                                                                                                                                                                                     The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                    Homer MJ;
                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                     New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                     (212)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B. microti MN-10/BMNI-17/BMNI-15 fusion protein SEQ ID NO: 87.
                                                                                                                                                  Sleath PR, McNeill PD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  McNeill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Babesiosis; rodent parasite; tick-borne illness; antigen; disease diagnosis; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                      Length
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 139; DB 23; 100.0%; Pred. No. 1.2e-12;
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                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
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                                                                                                                                                                                                                                                  Claim 35; Page 160-163; 195pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAB30231 standard; Protein; 1132 AA
                                                                                                                                                  Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houghton RL,
                                                            2000US-0605724.
2000US-0656688.
2000US-0685436.
2000US-0737178.
                              09-MAY-2001; 2001WO-US15192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-APR-2000; 2000WO-US09136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-APR-1999; 99US-0286488
17-MAR-2000; 2000US-0528784
                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local Similarity 100.0
Matches 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-FEB-2001 (first.entry)
                                                                                                                                                  Lodes MJ,
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                                                                                                                              (CORI-) CORIXA CORP.
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                                                                                                                                                                                                                                                                                                                                               677 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200060090-A1.
                                                            27-JUN-2000;
07-SEP-2000;
10-OCT-2000;
13-DEC-2000;
26-FEB-2001;
                                                   10-MAY-2000;
          15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-OCT-2000
                                                                                                                                                            Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Babesia sp.
Synthetic.
                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                                                  Reed SG,
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qq
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                                                                                                                                                                                                              The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis,
New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 139; DB 21; 100.0%; Pred. No. 2.1e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                         Example 7; Page 112-116; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: July 16, 2003, 17:46:46 Job time: 8.27825 secs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity , 100.0
                                                                                                                                                                                                                                                                                                                                                                                                                               1132 AA;
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microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                 Protozoacide; vaccine; antigen; antigenic epitope; infection
                                                                                                                                 Babesia microti antigenic epitope fusion protein BaF-3.
                                   ABB88975 standard; Protein; 666 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2002-216691/27
                                                                                                                                                                                                 Babesia microti.
                                                                                                                                                                                                                                  WO200185947-A2
                                                                                                                                                                                                                                                                                                                                                                               10-OCT-2000; 213-DEC-2000; 26-FEB-2001; 2
                                                                                                                                                                                                                                                                                               09-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                27-JUN-2000;
07-SEP-2000;
                                                                                                                                                                                                                                                                                                                               10-MAY-2000;
                                                                                                                                                                                                                                                                15-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed SG, L
Secrist H;
                                                                    ABB88975;
   RESULT 13
ABB88975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB88989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                     Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                              parasite; tick-borne illness; antigen;
                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                McNeil1
                                                                                                                                                                                                                                                                                                                                                                                                              B. microti MN-10/BMNI-17 fusion protein SEQ ID NO: 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 139; DB 21;
100.0%; Pred. No. 1.1e-12;
ive 0; Mismatches 0;
                                                                                                                                 Score 139; DB 23;
Pred. No. 7.8e-13;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 7; Page 108-111; 118pp; English.
                                                                                                                                                                                                                    218 GKPNTNKSEKAERKSHDTQTTQEICE 243
                                                                                                                                                                                                1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                               disease diagnosis; disease prevention.
                                                                                                                                                                                                                                                                                                              AAB30230 standard; Protein; 666 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Houghton RL,
                                                                                                                                                                 ö
                                                                                                                                 100.0%;
100.0%;
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17-MAR-2000; 2000US-0528784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2000; 2000WO-US09136
                                                                                                                                                                                                                                                                                                                                                                             12-FEB-2001 (first entry)
                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-686939/67.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lodes MJ,
                                                                                                                            Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                Babesiosis; rodent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              666 AA;
                                                                                                  481 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200060090-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Babesia sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                               AAB30230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                            RESULT 12
AAB30230
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Homer MJ;

McNeill PD,

Sleath PR,

Houghton RL,

Lodes MJ,

2000US-0605724. 2000US-0656688. 2000US-0685436. 2000US-0737178.

2001US-0794764

2001WO-US15192

(first entry)

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                                    The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for
                                                                                                  diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                  ;
0
                                                                                                                                                                                                                          Length 666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Babesia microti antigenic epitope fusion protein BaF-5.
                                                                                                                                                                                                                          100.0%; Score 139; DB 23;
100.0%; Pred. No. 1.1e-12;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                   403 GKPNTNKSEKAERKSHDTQTTQEICE 428
Claim 35; Page 113-115; 195pp; English.
                                                                                                                                                                                                                                                                                                             1 GKPNTNKSEKAERKSHDTQTTQEICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB88989 standard; Protein; 677 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                               Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                     666 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Babesia microti,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200185947-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-JUN-2002
                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 14
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Gaps

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Indels

403

GKPNTNKSEKAERKSHDTQTTQEICE 26

Conservative

Local Similarity nes 26; Conserv

Matches

δ . d Homer MJ;

McNeill PD,

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The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to novel Babesia microti antigens and their
                                                                                                                                                                          New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New Babesia microti antigens, useful for diagnosing and treating B microti infection, and as component of a composition for enhancing immune response against B. microti infections \, -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.0%; Score 139; DB 23;
ilarity 100.0%; Pred. No. 7.1e-13;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Babesia microti antigenic epitope fusion protein.
                                                                 Sleath PR,
                                                                                                                                                                                                                     immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                             Example 1; Page 92-93; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 191-192; 195pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ¥.
                                                                 Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB89025 standard; Protein; 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000US-0605724.
2000US-0656688.
2000US-0685436.
2000US-0737178.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAY-2001; 2001WO-US15192
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                                                                 Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lodes MJ,
                        (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP
                                                                                                                               WPI; 2002-216691/27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
les 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                              445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Babesia microti.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-SEP-2000;
10-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-DEC-2000;
26-FEB-2001;
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                                                                                     Secrist H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secrist H:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                              Reed SG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             polypeptides containing an antigenic portion of Babesia microti
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protozoacide; vaccine; antigen; antigenic epitope; infection.
B. microti BMNI-17 antigen reverse complement SEQ ID NO: 38.
                                                                                                                                                                                                                                                                                                                                                                                             McNeill PD;
                                          parasite; tick-borne illness; antigen; disease prevention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match 100.0%; Score 139; DB 21; Local Similarity 100.0%; Pred. No. 7.1e-13; les 26; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                          Sleath PR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Page 86-87; 118pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babesia microti antigen epitope #1.
                                                                                                                                                                                                                                                                                                                                                                                          Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABB88952 standard; Protein; 445
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2000US-0656688.
2000US-0685436.
2000US-0737178.
2001US-0794764.
                                                                                                                                                                                                                                      05-APR-2000; 2000WO-US09136
                                                                                                                                                                                                                                                                               05-APR-1999; 99US-0286488
17-MAR-2000; 2000US-0528784
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                                                                                                                                                                                                                                                                                                                                                                                          Lodes MJ,
                                                                                                                                                                                                                                                                                                                                              (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2000-686939/67
                                          Babesiosis; rodent
disease diagnosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   445 AA;
                                                                                                         Babesia microti
                                                                                                                                                 WO200060090-A1
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13-DEC-2000;
26-FEB-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .5-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                          Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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RESULT

ò g McNeill PD,

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Gaps

; 0

Indels

Length 445;

Gaps

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Babesia microti BMNI-17 complement antigen sequence.
                                                                                              1 GKPNTNKSEKAERKSHDTQTTQEICE 26
    Example 1; Page 103; 195pp; English.
                                                                                                                                                                                                                                                                                                                             Claim 1; Page 77-79; 113pp; English.
                                                                                                                               AAW56298 standard; Protein; 445 AA
                                                                                                                                                                                                                                        97US-0845258.
                                                                                                                                                                                                                              97EP-0117067
                                                                                                                                                      28-SEP-1998 (first entry)
                                                                             26; Conservative
                                                                                                                                                                                                                                                                     Houghton R, Lodes MJ,
                                                                                                                                                                                                                                                                               WPI; 1998-195465/18.
                                                                                                                                                                                                                                                          (CORI-) CORIXA CORP.
                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  445 AA;
                                                       275 AA;
                                                                                                                                                                                                                                                                                     N-PSDB; AAV22753
                                                                                                                                                                                             Babesia microti
                                                                                                                                                                                                                              01-OCT-1997;
                                                                                                                                                                                                                                         24-APR-1997;
                                                                                                                                                                                                                                              01-OCT-1996;
                                                                                                                                                                                                                   08-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                  Seguence
                                                       Sequence
                                                                                                                                           AAW56298;
                                                                             Matches
                                                                                                                    RESULT 7
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Reed SG,

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Babesia microti antigen BMNI-17 complementary open reading frame protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      microti infections. The present sequence encodes a B.microti antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                       Babesia microti; antigen; immunogen; diagnosis; infection; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 445;
                     Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Reed SG;
                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 139; DB 20;
llarity 100.0%; Pred. No. 7.1e-13;
Conservative 0; Mismatches 0;
                   Score 139; DB 19;
Pred. No. 7.1e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Persing D,
                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated Babesia microti polypeptides
                                                                                                                          182 GKPNTNKSEKAERKSHDTQTTQEICE 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 GKPNTNKSEKAERKSHDTQTTQEICE 207
                                                                                                    1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 91-92; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB30207 standard; Protein; 445 AA.
                                                                                                                                                                                                                                                       AAY24358 standard; Protein; 445 AA
                                                             ;
0
                   100.0%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98WO-US26437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97US-0990571.
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                                                                                                                                                                                                                                                                                                                                      (first entry)
Query Match
Best Local Similarity 100.0
There 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Houghton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (CORI-) CORIXA CORP. (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                             immunity; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-385612/32.
N-PSDB; AAX90012.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                445 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Babesia microti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9929869-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-DEC-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bruinsma E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-FEB-2001
                                                                                                                                                                                                                                                                                                                                      16-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-JUN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sleath PR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB30207;
                                                                                                                                                                                                                                                                                               AAY24358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 9
                                                                                                                                                                                                              RESULT 8
                                                                                                                                                                                                                                      AAY24358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB30207
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                                                        The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence is that of a polypeptide comprising at least one antigent portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:

(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to protect against infection, especially when formulated with an adjuvant. The new diagnostic methods allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehriichhosis) that have similar symptoms but require different treatments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptides comprising Babesia microti antigens and their immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of infection and in protective vaccines
                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                       Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.
                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                   100.0%; Score 139; DB 23;
100.0%; Pred. No. 4.1e-13;
ive 0; Mismatches 0;
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Gaps

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The present invention is related to the isolation of antigenic sequences from the rodent parasite Babesia microti. This organism is transmitted to humans by the same tick which transmits Lyme disease and ehrlichiosis. The organism causes a malaria-like infection known as babesiosis. The sequences identified by this invention can be used in the diagnosis, prevention and treatment of babesiosis.
                                                                                                                                                                                                                                                New polypeptides containing an antigenic portion of Babesia microti antigen and DNAs encoding the polypeptides, useful for diagnosing, treating or preventing B. microti infection, or for inducing protective immunity in a patient
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sleath PR, McNeill PD,
                                                                                                                                                          Sleath PR, McNeill PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 139; DB 21;
100.0%; Pred. No. 4.1e-13;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               218 GKPNTNKSEKAERKSHDTQTTQEICE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                            Example 1; Page 98; 118pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Houghton RL,
                                                                                                                                                          Houghton RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Babesia microti antigen BMNI-20.
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2000US-0656688.
2000US-0685436.
2000US-0737178.
2001US-0794764.
05-APR-2000; 2000WO-US09136
                                          05-APR-1999; 99US-0286488
17-MAR-2000; 2000US-0528784
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09-MAY-2001; 2001WO-US15192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 26; Conservative
                                                                                                             (CORI-) CORIXA CORP.
                                                                                                                                                          Lodes MJ,
                                                                                                                                                                                                    WPI; 2000-686939/67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-216691/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Babesia microti.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200185947-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07-SEP-2000;
10-OCT-2000;
13-DEC-2000;
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                                                                                                                                                       Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABB88962;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Reed SG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABB88962
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                                                                                                                                                   Babesia microti antigen BMNI-20 complementary open reading frame protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention describes isolated polypeptides comprising specific immunogenic portions of Babesia microti. AAX88983 to AAX88994 encode specifically claimed B. microti immunogenic proteins, and AAV24327 to AAY2432 represent these proteins. B. microti polypeptides and nucleic acids can be used for detecting B. microti infections. They can also be used in vaccines for inducing protective immunity against B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microti infections. The present sequence represents a B.microti antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                               Babesia microti; antigen; immunogen; diagnosis; infection; vaccine; immunity; detection.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Persing D, Reed SG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Babesiosis; rodent parasite; tick-borne illness; antigen; disease diagnosis; disease prevention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 139; DB 20;
100.0%; Pred. No. 4.1e-13;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated Babesia microti polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Page 109-110; 126pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  218 GKPNTNKSEKAERKSHDTQTTQEICE 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GKPNTNKSEKAERKSHDTQTTQEICE 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B. microti clone antigen SEQ ID NO: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lodes MJ,
                AAY24365 standard; Protein; 275 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB30217 standard; Protein; 275
                                                                                                                                                                                                                                                                                                                                                                                                   98WO-US26437
                                                                                                                                                                                                                                                                                                                                                                                                                                                97US-0990571
                                                                                                         (first entry)
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(MAYO-) MAYO FOUNDATION

Bruinsma E,

Sleath PR;

(CORI-) CORIXA CORP

Babesia microti

16-SEP-1999

AAY24365;

AAY24365

WO9929869-A1

17-JUN-1999

11-DEC-1998;

11-DEC-1997;

WPI; 1999-385612/32.

N-PSDB; AAX90017

Local Similarity

Matches

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XX DY XX

Query Match

275 AA;

Seguence

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Gaps

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Homer MJ;

'a microti. -A1.

Gaps

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The sequence is that of a polypeptide comprising at least one antigenic portion of a Babesia microti antigen. It can be used to diagnose B. microti infection by detecting specific antibodies in usual immunoassays. Infection can also be diagnosed using:
(a) primers or probes derived from the coding sequence, in standard amplification or hybridisation tests, or (b) using antibodies to detect the corresponding antigen. It is also useful in vaccines to proceet against infection, especially when formulated with an adjuvant. The new diagnostic methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Polypeptides comprising Babesia microti antigens and their . immunogenic fragments or epitopes - and related nucleic acid, vectors, transformed cells and antibodies, useful for diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   allow rapid differentiation between B. microti infection and other tick-borne diseases (Lyme disease and ehrlichiosis) that have similar symptoms but require different treatments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 275;
                                                                                                                                                                                                                                                                                            antigen; detection; diagnosis; vaccine; tick-borne disease; differentiation; Lyme disease; ehrlichiosis.
             Length
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                                         Indels
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100.0%; Pred. No. 4.1e-13;
iive 0; Mismatches 0;
            Score 139; DB 23;
Pred. No. 5.9e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sleath PR;
                                         Mismatches
                                                                                                                                                                                                                                                                  Babesia microti BMNI-20 antigen sequence.
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                                                                                                 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           infection and in protective vaccines
                                                                     Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Reed SG,
                                                                                                                                                                           AAW56303 standard; Protein; 275
                                         ..
            100.0%;
ilarity 100.0%;
Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  97EP-0117067
                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0845258.
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hes 26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lodes MJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1998-195465/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (CORI-) CORIXA CORP
         Query Match
Best Local Similarity
Matches 26; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               275 AA;
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                                                                                                                                                                                                                                                                                                                                            Babesia microti.
                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1997;
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                                                                                                                                                                                                                                    28-SEP-1998
                                                                                                                                                                                                                                                                                                                                                                        EP834567-A2
                                                                                                                                                                                                                                                                                                                                                                                                     08-APR-1998
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                                                                                                                                                                                                          AAW56303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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Matches
                                                                                                                                               RESULT 3
                                                                                                                                                                AAW56303
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                                                                                                 The present invention relates to novel Babesia microti antigens and their coding sequences. The B. microti antigens, antigenic epitopes of such antigens, and compositions comprising such antigens are useful for diagnosing and treating B. microti infection. The compositions are especially useful for enhancing immune response against B. microti infection. The present sequence was used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homer MJ;
                                                                                                                                                                                                                                                                     Gaps
            New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Babesia microti antigens, useful for diagnosing and treating B. microti infection, and as component of a composition for enhancing immune response against B. microti infections
                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Protozoacide; vaccine; antigen; antigenic epitope; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McNeill PD,
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                   100.0%; Score 139; DB 23;
100.0%; Pred. No. 2.8e-14;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sleath PR,
                                                                                                                                                                                                                                                                                                              1 GKPNTNKSEKAERKSHDTQTTQEICE 26
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## SUMMARIES

			Description	Babesia microti an	Babesia microti an	Babesia microti BM	Babesia microti an	B. microti clone a	Babesia microt1 an	Babesia microti BM	Babesia microti an	B, microti BMNI-17	Babesia microti an
SUMMAKIES		í	ID.	٠,	ABB89012	AAW56303	AAY24365	AAB30217	ABB88962	AAW56298	AAY24358	AAB30207	ABB88952
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		Query	Length	26	20	275	275	275	275	445	445	445	445
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	139 100.0 481 23 AB 139 100.0 666 21 AA 139 100.0 666 23 AB 139 100.0 666 23 AB 139 100.0 1132 23 AB 139 100.0 1132 23 AB 15.1 25 23 AB 15.3 32 20 AB 15.3 36.7 25 23 AB 15.7 25 AB 15.7	ALIGNMENTS  UT 1  9013  ABB89013 standard; Peptide; 26 AA.  ABB89013;  20-JUN-2002 (first entry)  Babesia microti antigen BMNI-17 peptide BM  Protozoacide; vaccine; antigen; antigenic  Babesla microti.  WO200185947-A2.  15-NOV-2001.  09-MAY-2000; 2000US-0569098.  27-JUN-2000; 2000US-0569098.  27-JUN-2000; 2000US-0566688.  10-OCT-2000; 2000US-0656688.  11-DEC-2000; 2000US-0696688.  13-DEC-2000; 2000US-0696688.  13-DEC-2000; 2000US-0794764.  (CORI-) CORIXA CORP.  Reed SG, Lodes MJ, Houghton RL, Sleath Secrist H;  WPI; 2002-216691/27.